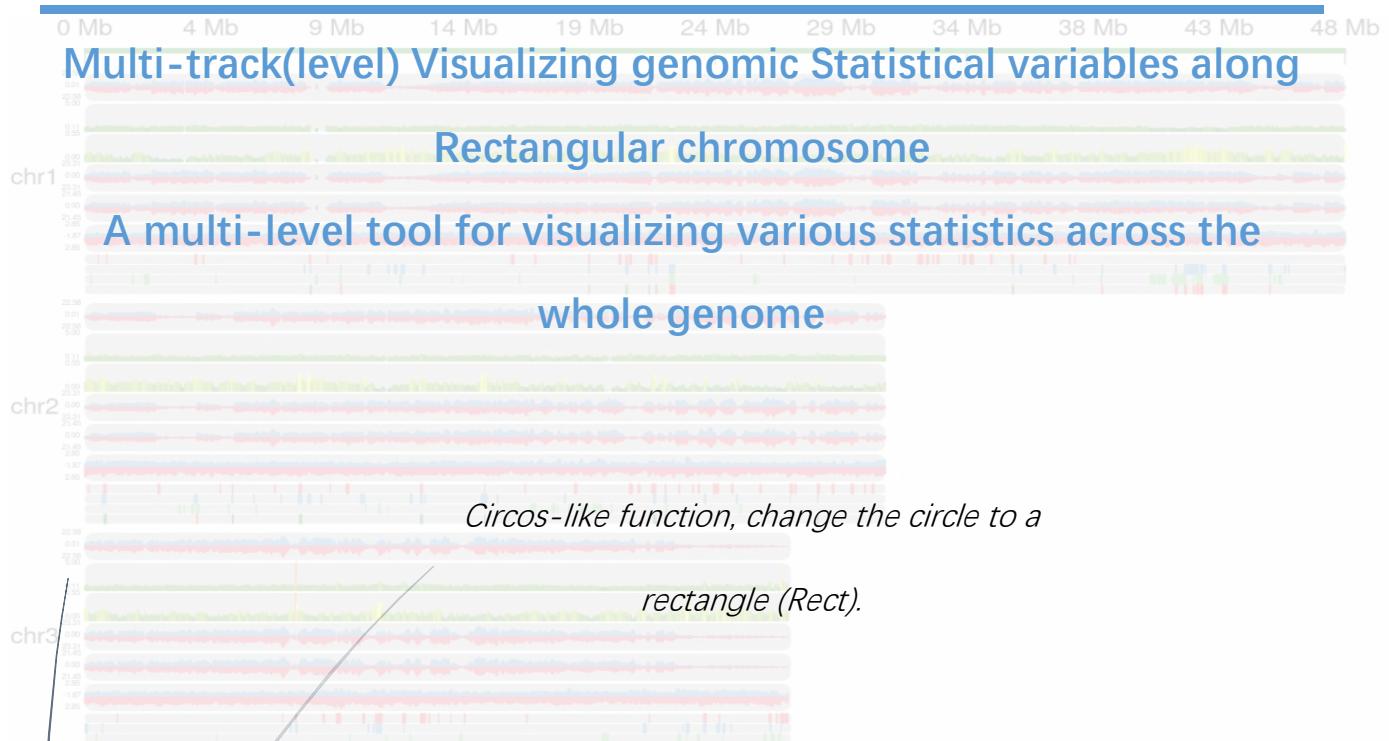


使用手册

RectChr



Version 1.42 User Documentation

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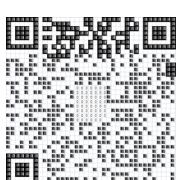


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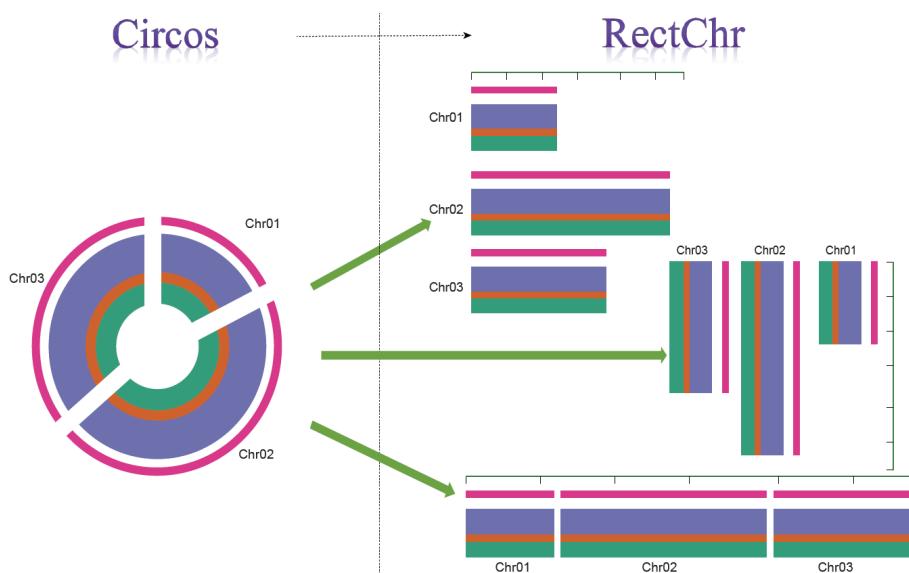
1. Introduction

RectChr is a multi-level visualization tool that focuses on the chromosome (Chr) level. It uses a wide variety of visualization elements, including points, shapes, lines, histograms, heatmaps, highlights, text, rainbow links, self-links, dynamic heatmaps, dynamic histograms, ridgelines, etc., and cleverly **combines colors to use** [scatter/point, shape, line] (line), histogram, heatmap/highlights, heatmap /highlights), text, ridgeline, PairWiseLink, self-connect (LinkS), heatmapAnimated, and histAnimated], which visually presents various statistical variables, so as to realize the visual display of statistics in different regions on each chromosome. Users can quickly and intuitively gain insight into data patterns and identify analysis results through this tool.

One of the significant advantages of this tool is its high degree of flexibility. Users can freely combine various visualization elements according to their own needs and modify relevant parameters independently. It is used in a very similar way to the classic **Circos** tool, but with an innovative twist. The visualization that circos can achieve is **the same as that RectChr can** achieve, except that RectChr transforms the traditional circle diagram form into a rectangle (which can be placed horizontally or vertically). In addition, users can also match the colors and other styles of each layer by themselves. **To put it simply, circos can be drawn, and everything can be drawn here, but the circle diagram can be changed to a rectangular shape (can be placed horizontally or vertically).**

Not only that, but RectChr also provides some default configurations that further simplify the usage process. For example, when dealing with common analyses such as SNP GC density, users can easily visualize it by simply entering the relevant files, making it truly easy to use.

The program is for some basic students, if the **novice can't understand it, forget it.**



[Program provided](#) After 10 different application scenario examples, [Know the columnConfigurations](#) and instructions from some users have also been collected.

New features in each version

- A. 1.29 RectChr of it [New feature ColorBrewer](#) Add a color palette
- B. 1.30 fix 1.29 introduced, in the special data *TopVHigh/TopVLow* must be manually set to the bug, otherwise an error will be reported
- C. 1.31 Added a new drawing [method shape function](#), which allows you to draw a total of [12 types of graphics](#)
- D. 1.33 Added a new way of mapping ridgeline, i.e. ridgeline function [Click to view the new feature description](#).
- E. 1.35 added *zoom_regionZoom* in to see only the function of a certain area, with it [Click here to see the new features](#).
- F. 1.39 a: Brand new parameters that provide ParaOld2New.pl The old configuration can be moved to the new configuration
 - B: Shape function provides multiple left and right semicircles
 - c: Adding *track_shift_y* allows you to draw multiple *plots on the same layer_type*
- G. 1.41 Legend adds a total of 13 layout methods

2. Function introduction

RectChr has rich and flexible visualization capabilities, and here is a brief description of its features:

- 1) **Chromosome layout customization:** You can freely set the placement direction (*chr_orientation*) and order (*chr_order*) of chromosomes, and you can choose horizontal or vertical orientation. At the same time, you can also define the gap between chromosomes (*padding_ratio*), the height of each layer (*track_height*), and the background color (*background_color*).
- 2) **Multi-layer drawing structure:** Each chromosome can define a multi-layer structure, the number of layers is determined by *track_num* (level), and each layer can be displayed in different drawing methods.
- 3) **Diverse drawing methods:** 12 drawing types (*plot_type are available*), including scatter/point, shape, line, histogram, heatmap, highlights, text, ridgeline, PairWiseLink, LinkS, HeatmapAnimated and histAnimated to meet different visualization needs.
- 4) **Color and Data Range Adjustments:** Supports custom modifications to color artboards

(such as colormap_brewer_name), **color gradients, and aliquots** (colormap_nlevels). At the same time, the range of data can be limited, for example by *parameters such as YMax, upper_outlier_ratio, cap_max_value, etc.*

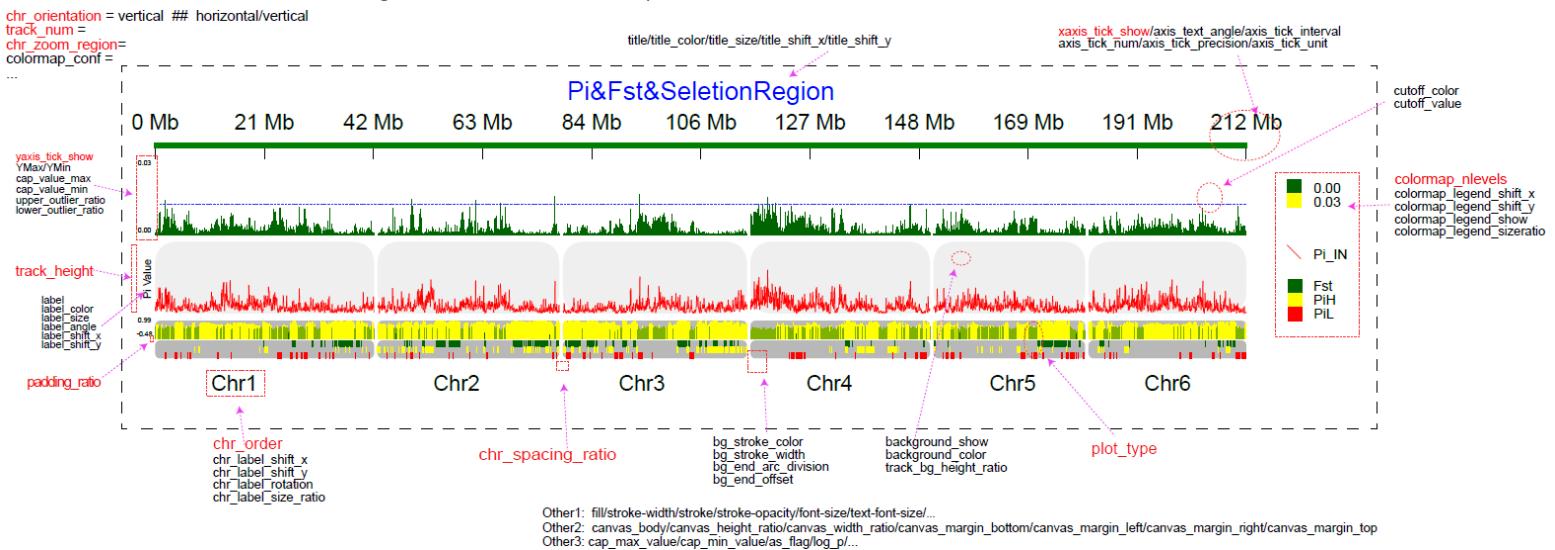
5) Unified input format: The input format is unified, and it is very easy to specify statistics, such as *show_columns = File2:4*, where the first three columns represent the region, and File2:4 uses the fourth column of the second file as the graphing statistics.

6) Area Magnification Function: Using *the zoom_region* parameter, it is possible to zoom in on specific areas, making it easy to focus on details.

7) Open customization of parameters: All parameters are open to the public, and users can modify the details according to their needs.

8) ...

Here is a diagram of some control parameters:

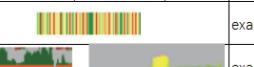
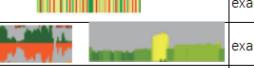
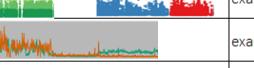
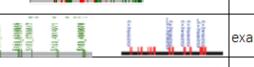
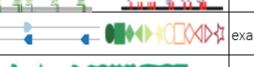
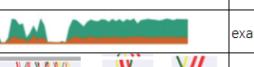
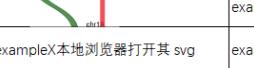


Some important parameters are marked in red.

3. Examples of drawing methods

Here are some examples of basic usage tutorials, and the specific data and configuration can be found in the Basic_Tutorials of the software

The following is a simple list of 12 drawing methods:

顺序	绘图类型	plot_type	说明	示例图(Basic_Tutorials)	位置
1	热图	heatmap	用颜色深浅来表示数据密度或数值大小的图表。能直观呈现数据的分布和变化趋势。常用于展示基因表达量、SNP密度等数据。		example01
2	柱状图	histogram	以柱状图为变量的统计图表，通过柱子的高度和颜色来展示数据的数量、频率等统计量。常用于比较不同类别之间的数据差异(两个群体的pi)		example02
3	点	scatter/point	用点的高低和颜色来表示变量大小的图表，每个点代表一个数据点。可用于发现数据的分布模式、异常值以及变量之间的相关性，如GWAS。		example03
4	线	line	通过线条连接各个数据点，展示数据随在chr上各区域的变化趋势。常用于分析数据的连续性变化。如Fst等。		example04
5	高亮显示	highlights	对特定的数据区域或元素进行突出显示颜色，使其在图表中更加醒目，便于用户关注关键信息。如看丝粒和区域		example05
6	文本	text	在图表中添加文字说明(可带颜色)，用于标注数据点、解释图表含义、提供额外信息等。增强图表的可读性和可理解性。		example06
7	形状	shape	用形状(如圆形、方形、三角形等共15种)来表示数据，形状的类型、颜色属性可对应不同的数据特征。能以独特的方式展示数据信息。		example07
8	山脊线	ridgeline	一种特殊的可视化图表，将多个分布曲线堆叠在一起，类似山脉的山脊，用于比较多分布的形状、中心位置和离散程度。		example08
9	彩虹链接	pairwiselink pairwiselinkV2	用于展示chr上两个点中数据对象之间的关联关系，通常用贝塞尔曲线条连接相关对象，线条的颜色、高低等可表示关联的强度或其他属性。		example09
10	自连接	LinkS	用于展示chr两个区域中数据对象之间的关联关系，通常用彩色的线条连接相关对象，线条的颜色、高低等可表示关联的强度或其他属性。		example10
11	动态热图	heatmapAnimated	动态热图，在SVG文件中heatmap，颜色随时间变化，能够动态展示数据在不同时间点(状态)的分布和变化情况。较少用到	见 exampleX本地浏览器打开其svg	example11
12	动态直方图	histAnimated	动态的柱状图，在SVG文件中柱子的高度或颜色随时间变化，可用于展示数据随时间(状态)的动态变化过程。较少用到	见 exampleX本地浏览器打开其svg	example12
13	其它	OthersNA	若输入的绘图类型不是关键词，则不进行绘图，仅显示背景条，起到占位和区分的作用。		-

In order to show the differences between these drawing categories, in Basic_Tutorials the `track_num=1` (several circles of circos) layer is the main layer, some basic usage and tutorials are examples, and the specific related data and configuration can be found in the software **Basic_Tutorials** in the example directory

3.1 Heatmap mapping example

Example 1

Input File Format: [#Chr Stat End Flag] , a total of four columns, of which the Flag column is the value of the statistic in this area, which can be an integer, a decimal, or a string . Among them, the figure below uses binboxThe size number can be indicated by color.

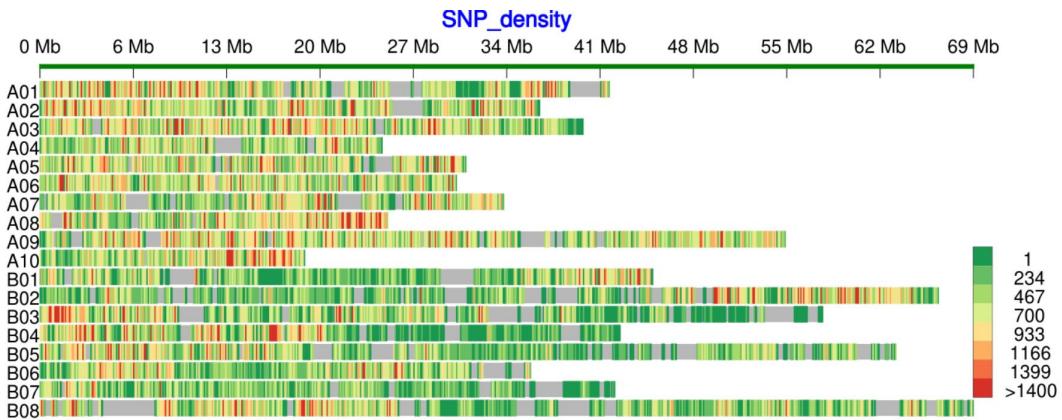
Density Diagram:

- 1 Chr column, default `chr_orientation=vertical`
- 2 Several layers (a few circles of cir cos), `track_num =1`, by default according to the number of file columns
- 3 The mapping method `plot_type` defaults to heatmap
- 4 Data column: Default is `show_columns = File1:4` File The 4th column of File1 is the graphing data

Therefore, they can be defaulted and can be configured minimally, just pass in the file

```
SetParaFor= global
File1= ./SNP.dis.gz
```

See Basic_Tutorials/example01 for specific configurations and data



In order to make it very convenient for users to draw these graphs, we provide a small perl script (`CountBinNumPlot.pl`) in the corresponding directory `example01_Density_heatmap`, which can be used from vcf to the SNP density map in the above picture in one step. The gene density distribution force can also be obtained from the GFF file in one step, as detailed in the field shadow application `example01` below.

```
##### run SNP_density for VCF File example #####
#perl .. /bin/script/CountBinNumPlot.pl -InFile in.vcf.gz -OutPut SNP_density
#perl .. /bin/script/CountBinNumPlot.pl -InFile in.vcf.gz -OutPut SNP_density -BinSize 10000
### run gene_density for gFF File example #####
#cat Ref.gff |awk '$3=="mRNA"' >mRNA.gff
#perl .. /bin/script/CountBinNumPlot.pl -InFile mRNA.gff -SiteColumn 4 -OutPut gene_density
```

Example 2

`track_num` If there is no setting, it will be judged based on the number of columns in `File1`

For example, `mat.fst(chr start end Flag1 ... Flag12)`

Then the default `track_num = 12` for each trackX corresponds to the value of FlagX

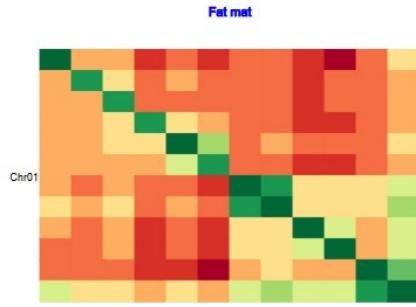
Then the following unified Ymax Ymin, etc., you can draw a heatmap map,

```
SetParaFor= global
File1= mat.fst
title= "Fat mat"
#track_num =12 ## The default is to subtract 3 based on the number of columns in File1
canvas_body=360 ## 12 columns*20 mat.fst

xaxis_tick_show=0 ## does not show the x-axis
SetParaFor= trackALL
plot_type = heatmap ## The mapping method is heatmap, text
upper_outlier_ratio=1.0
colormap_nlevels=10
Ymax=0.65 ##设置此层(ValueX) maximum value, default automatic, display range
Ymin=0 ##设置此层(ValueX) is the minimum value, the default automatic, the range displayed
colormap_legend_show=0
```

The results are as follows:





3.2 Histogram drawing example

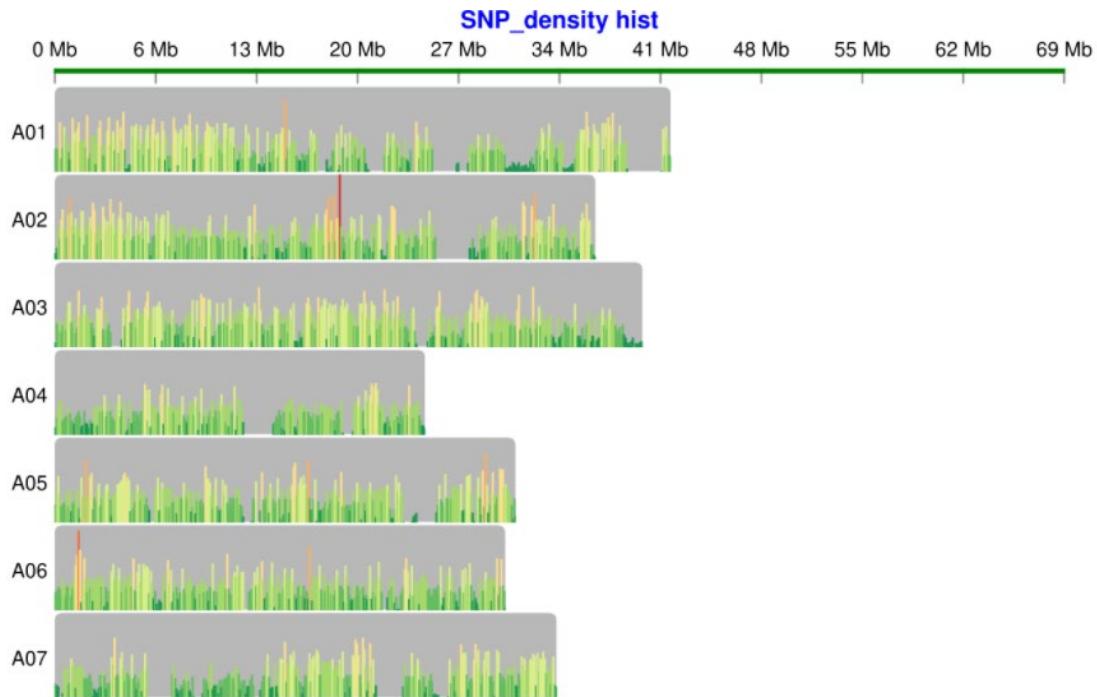
Example 1

The data is the same as example01_Density_heatmap

Density Diagram:

- 1 Chr columns, default vertical
- 2 Several layers (a few circles of cir cos), *track_num* =1, by default according to the number of file columns
- 3 The mapping method *plot_type* is changed to hist
- 4 The height of the current layer (i.e., the orbital height) is increased by *track_height* = 100

See Basic_Tutorials/example02 for specific configurations and data



Example 2

The following configuration should also be made on the top

- 1 Change the chr permutation from vertical to horizontal *chr_orientation=horizontal*

2 The colors don't want gradients.

Number of color gradient levels : *colormap_nlevels* = 3

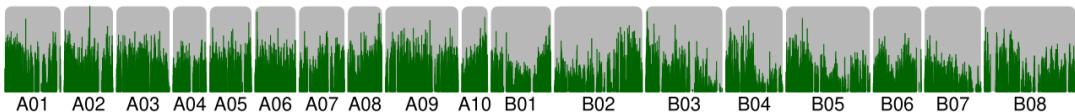
Tricolor gradient is changed to the same value

```
colormap_low_color = "#FFFF00" ## The color corresponding to the lowest value
colormap_mid_color = "#FFFF00" ## The color corresponding to the middle value
colormap_high_color = "#FF0000"
colormap_legend_show=0 ## does not display gradient bars, does not display legends
```

5 The x-axis is not displayed

xaxis_tick_show=0 # does not show the x-axis

You can get the following figure:

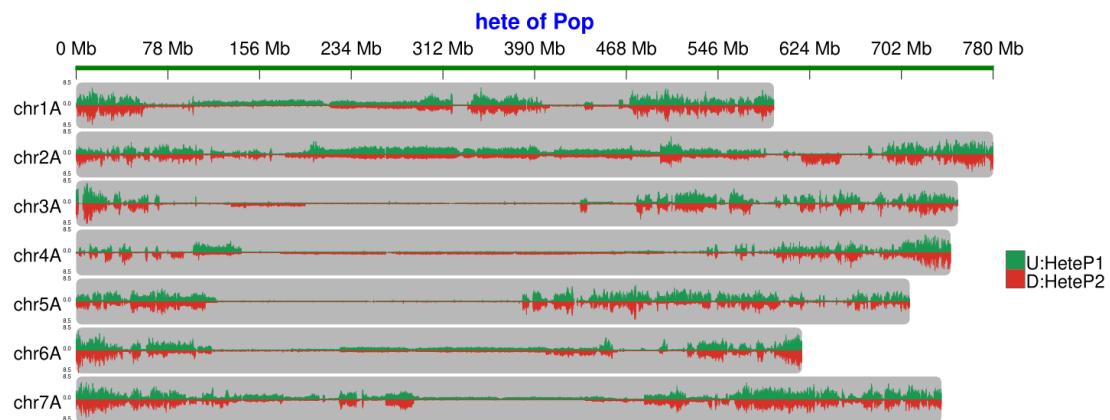


Example 3

On the same track, sometimes for convenience, you can also draw two columns of data and draw two hists, which will be centered, one up and one down:

Data columns: The default is *show_columns*= File1:6, and the 6th and 7th columns of File 7 are the graphing data, which is used to draw the upper and lower histograms

```
SetParaFor = track1 ## to start processing the layer 1 parameters
plot_type = hist ## Drawing type: histogram
show_columns = File1:6,7 ## Draw the upper and lower histograms with the number of columns 6,7 of File2
yaxis_tick_show=1 ## Displays the y-axis value
track_height=60 ## The track height is higher
#bg_end_arc_division=8 ## Background edge curvature, the larger the value, the smaller the curvature
```



3.3 Scatter(point) drawing example

Example 1

GWAS map points, two layers, one layer high, one layer low. The color of the dots is related to the high and low defaults, how to configure:

```
track_num = 2 ## There are two tracks (layers).
SetParaFor=track1 ## Let's start processing the layer 1 parameter processing
plot_type = point ## Mapping method scatter
show_columns= File1:4 ##把 file1 的第四列用散点图形式画出来)
track_height=100 ## The width of the first layer is adjusted to the height point
log_p=1 ##0-log() to take the log
background_color="#FFFFFF" ##背景为白色, there is no painting
```

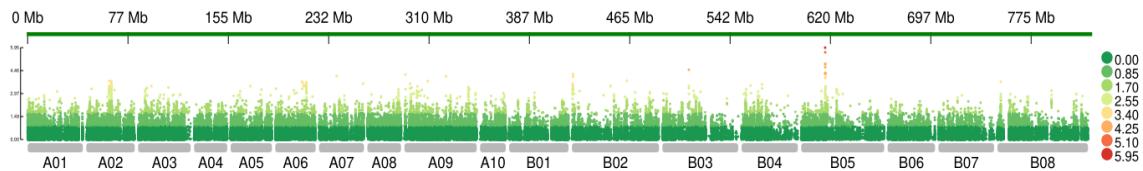
```

yaxis_tick_show=1 ##显示左边数值
padding_ratio=0.04 ##和 the next layer of track is empty and white
track_point_size=1.2 ##散点的大小按默认放大

SetParaFor=track2 ## This layer does not draw anything, only the background bar
show_columns= File1:4
track_height=10
plot_type = EEE ## Nothing is drawn, empty, only background bars

```

The following figure can be obtained:



Example 2

As shown in the Manhattan diagram above, but the color is solved by the level of the value, how to change it to **the color of chr?** Let's talk about a point here: for points and heat maps and columns

A: The color of the point when *ShowColumn = File1:4* is based on the value of the fourth column of File1 according to the principle of equal parts of the color

B: When *ShowColumn = File1:4 File2:4 File2:5*, then column 4 of File1 is the color A; Column 4 of File2 is color B; The fifth column of File2 is color C;

```

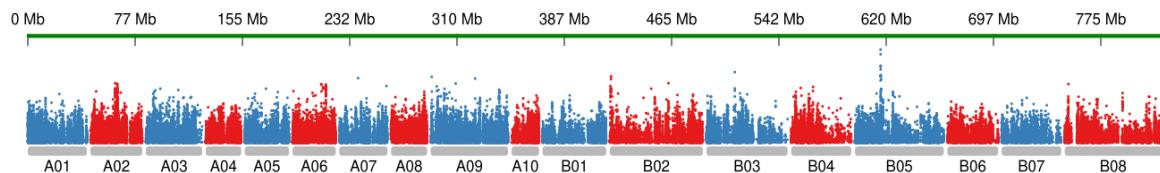
zcat Gwas.data.pvalue.gz |egrep "A02| A04| A06| A08| A10| B02| B04| B06| B08" > A.pvalue
zcat Gwas.data.pvalue.gz |egrep -v "A02| A04| A06| A08| A10| B02| B04| B06| B08" > B.pvalue

```

At the same time, it will be mainly changed here

```
ShowColumn = File2:4 File3:4 ## File2:4 Column Color A File3:4 Color B
```

The end result is as follows:

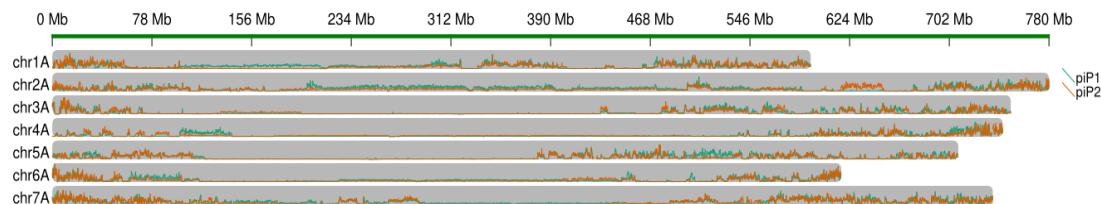


Additional note: If there are many GWAS sites, the SVG generated file will be larger, and the memory must be instantly large when converting to PNG. Note: Generally speaking, due to the linkage imbalance (LD) relationship, the adjacent SNP sites are often completely linked, that is, the corresponding Pvalue is the same (Y coordinate), and because the adjacent distance is small In the case of even 5000 on the canvas, in the 500M genome, canvas 1 represents 100k, and the distance at 1000bp on the canvas is only 0.01 difference (X coordinate). When all associated points are printed on the canvas, they are printed on the same point on the canvas. Based on this principle, RectChr 1.24 and above versions actually only print the last point, which can greatly reduce the file size of vector image svg, so as to achieve the goal of lossless compression.)

3.4 Lines diagram example

Example 1

```
SetParaFor= global
File1= ./poly.info.gz ##这个是必须输入文件路径
track_num=1 ##多少层, how many circles are similar to circos,
SetParaFor=track1 ##下面开始处理第 2 层参数处理
plot_type = lines ## The drawing method uses lines
show_columns = File1:4,5 ##把 file1 的第四和五列用 lines 图形式画出来
```



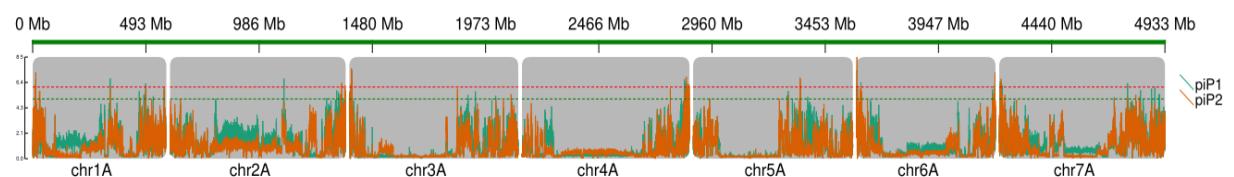
Example 2

For points, histograms, lines, etc., you can sometimes set multiple cutoff lines. The following is a cutoff line. As follows

Horizontally, add two cutoff lines

```
SetParaFor= global
File1= ./poly.info.gz ##这个是必须输入参数, enter the file path
track_num=1 ##多少层, how many circles are similar to circos,
chr_orientation = horizontal ## Chromosomes are arranged horizontally and horizontally
#canvas_height_ratio=0.8 ##Remove some of the blank space under the canvas

SetParaFor=track1 ##下面开始处理第 2 层参数处理
plot_type = lines ## The drawing method uses lines
show_columns= File1:4,5 ##把 file1 的第 4,5 列是画在 line drawing).
track_height=100
yaxis_tick_show=1 ##显示的 Y The start and end value of the axis
cutoff_y=6.0
cutoff2_y=5.0 ##cutoff_y, cutoff1_y, cutoff2_y 可以画三线
cutoff2_color=green ##cutoff 线 2 用 green 颜色
#bg_end_arc_division=8 ##背景边缘的曲度, the larger the curvature, the smaller the curvature
```



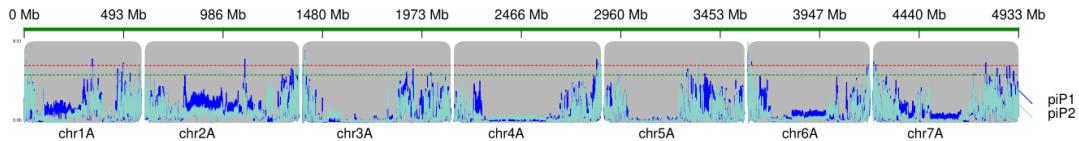
Example 3

Sometimes you can draw multiple lines, and if you want to show a highlighted one, you can use it

Use `line_colors_conf=line_colors.conf` to pass the colors of different lines, as shown below
line_colors the contents of .conf are as follows

1=blue

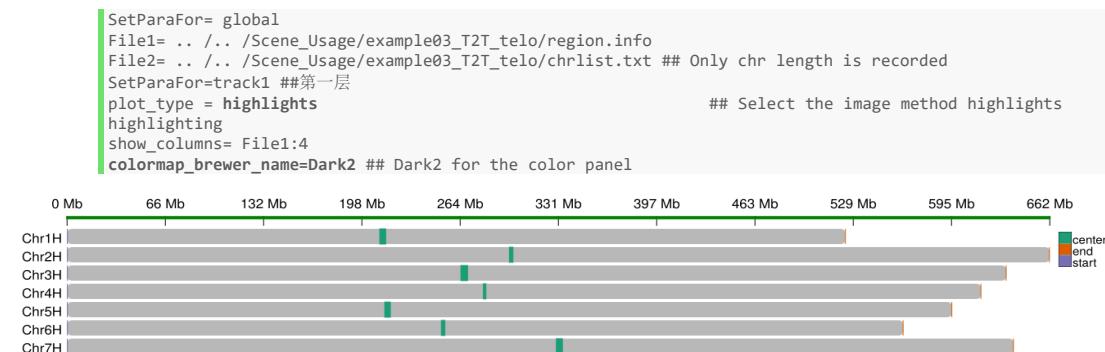
2="#1B9E77"



3.5 Highlights drawing examples

Example 1

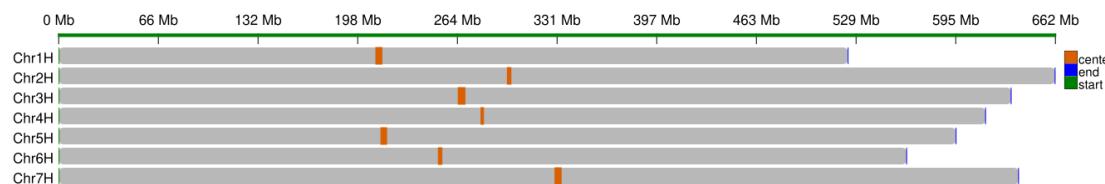
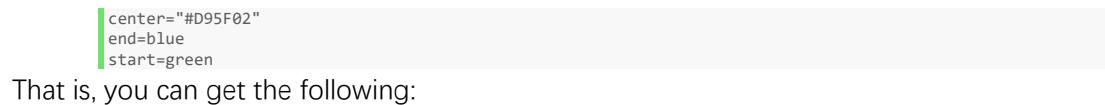
As follows:



Example 2

Sometimes you want to configure the color manually, you can customize the relationship between the value (Flag) and the color

colormap_conf = col.file This parameter can work in all plotting methods. The following file reads:

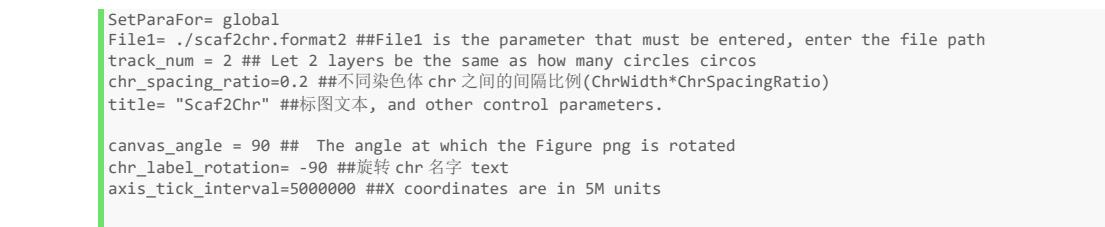


3.6 text diagram example

Example 1

Input format: #CHR Start End ScaName positive/negative

The following is mainly drawn with two layers of text and highlight.



```

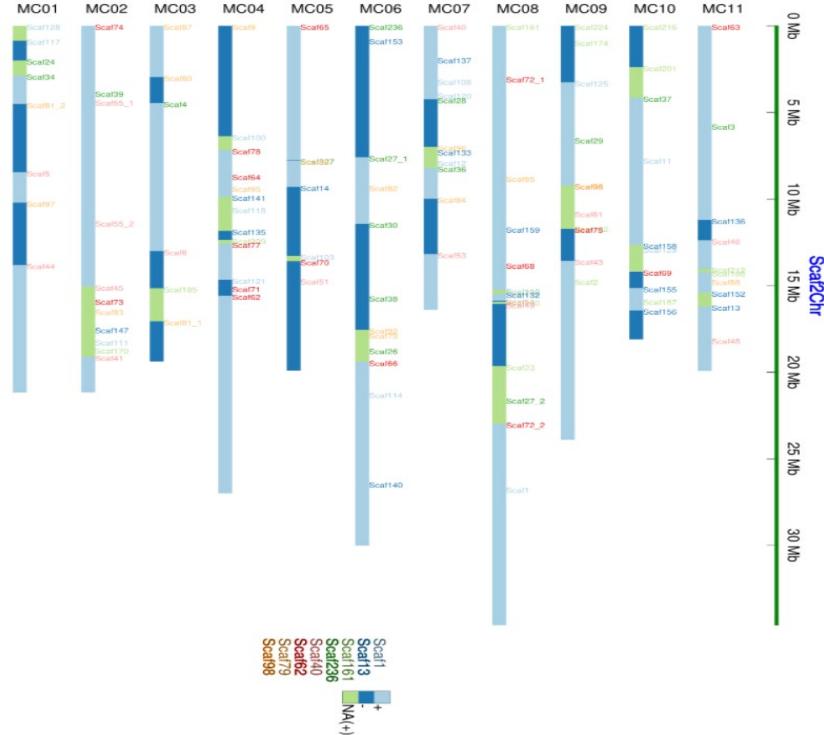
SetParaFor= trackALL ## The following is the processing of the initialization parameter SetParaFor
parameter processing
#colormap_legend_shift_x=-180
#colormap_legend_shift_y=-400

SetParaFor=track1 ##下面开始处理第 1 layer parameter processing
plot_type= text
show_columns= File1:4
track_height=80 ##放 text 的名字 Width Long Point
background_color="#FFFFFF" ##白色, i.e. no background
#track_text_angle=-90 ##旋转 90 度文字
text-font-size=14 ## Set the text size

SetParaFor=track2 ##下面开始处理第 2 layer parameter processing
plot_type= heatmap ##热图 indicates + -
show_columns = File1:7 ##把 file1 的第 7 columns are drawn in the form of scatter plots

```

See Example 1 for the configuration and usage of the input file format. The color of the text can be set to a uniform color by configuring



Example 2

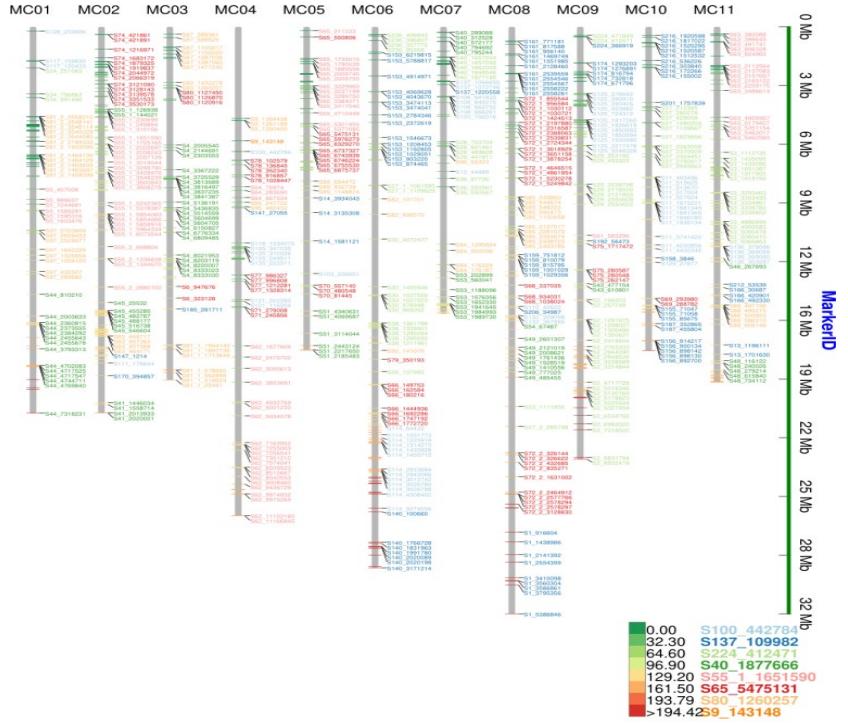
Genetic mapping

Input format: #CHR Start End ScaName positive/negative

The two layers are the combination of the text layer and the highlight layer. The width of the back color strip (track_bg_height_ratio) of the highlight layer is reduced by a point. The following parameters are added under the main SetParaFor=track2

```
track_bg_height_ratio=0.5 ## The width of the background becomes smaller
```





The back width, the configuration of the layer, and the color can be configured if they do not graduate

3.7 Shape drawing examples

Example 1

Input File A Format: [#Chr Stat End Flag] The Flag program will be based on the content of the Flag (*The same is true for other drawing methods*), judge for yourself whether it is a number or a character. Then the program sorts, such as the number in the shape will be differentiated according to the height, sometimes even if the content is data, if you want to be processed by shape, then just add parameters to the corresponding track **as_flag=factor** The four tracks are all according to the same data File1:4.

The second track is sorted by ASCII code, and the third track is by ASCII code, while customizing ShaPE.

There are a total of 16 shapes in shape, see track1 and track3 for correspondence

```

SetParaFor= global
File1= ./shape.type.data
track_num = 4 ## Four layers, compare the differences between different parameters of the four layers

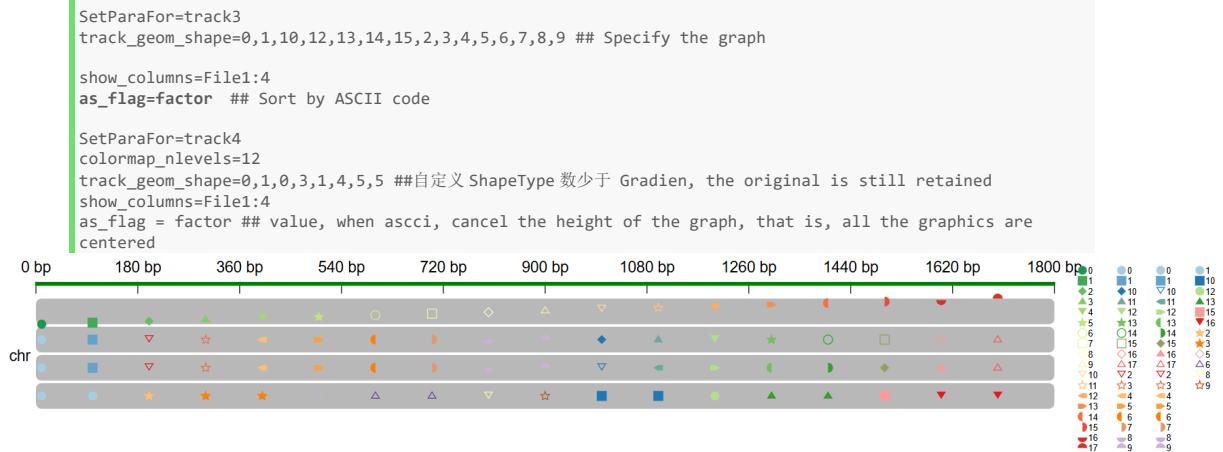
SetParaFor=trackALL
#colormap_legend_shift_x=20
#colormap_legend_shift_y=-40
plot_type = shape ##选图形作图方式
colormap_legend_sizeratio=0.8 ##渐变条的图 cases, a decrease of 0.8 times
track_geom_shape_size=5 ##图形的大小扩大 to 5
colormap_nlevels=18 ##18等份, exactly 18 data, one by one
track_height=30
padding_ratio = 0.1 ##同一染色体内相邻 track interval

SetParaFor=track1 ##第一层

SetParaFor=track2 ##第二层
as_flag=1
show_columns=File1:4

```

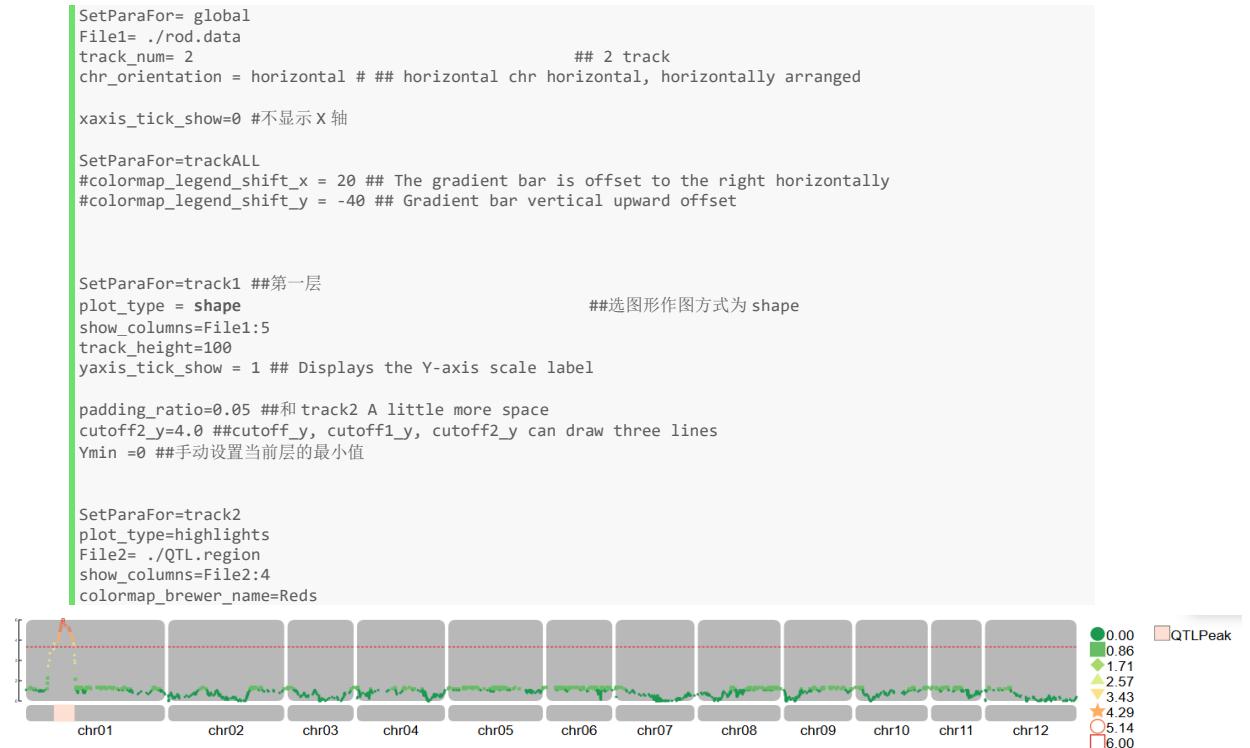




ShapeType starts from 0 to 17 corresponding to the shape

They are solid: circle, square, rhombus, upper triangle, lower triangle, pentagon, hollow: circle, square, rhombus, upper triangle, lower triangle, pentagon, left arrow, right arrow, left semicircle, right semicircle, upper semicircle and lower halfcircle.

Example 2



3.8 Ridgeline drawing example

Example 1

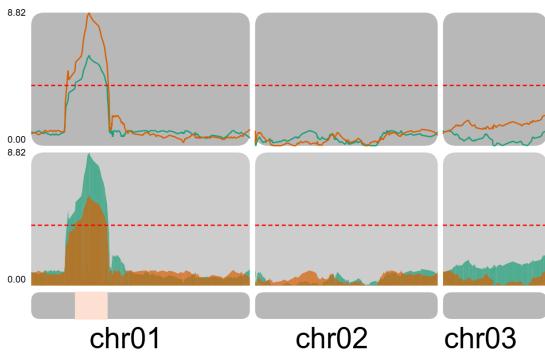
Ridgeline diagram, often another display format of line, the following is the difference after changing the line of track1 to ridgeline

At the same time, in order to set the transparency attribute of SVG, set the *stroke-opacity*

and fill-opacity to 0.7 in the track where the ridgeline is located

```
SetParaFor=track1 ## The first layer
plot_type = lines ##选图形作图方式 for lines lines
show_columns=File1:5,6
track_height=100
yaxis_tick_show = 1 ##显示 Y-axis scale label
#bg_end_arc_division=10
padding_ratio=0.05 ##和 track2 A little more space
cutoff2_y=4.0 ##cutoff_y, cutoff1_y, cutoff2_y can draw three lines
Ymin =0 ##手动设置当前层的最小值, overwrite the automatic calculation result

SetParaFor=track2 ## Layer 2
plot_type = ridgeline ##选图形作图方式山脊线
show_columns=File1:6,5 ##第六列先画 in front
track_height=100
yaxis_tick_show = 1 ##显示 Y-axis scale label
#bg_end_arc_division=10
padding_ratio=0.05 ##和 track2 A little more space
cutoff_y=4.0 ##cutoff_y Draw virtual, red by default
Ymin =0 ##手动设置当前层的最小值
colormap_brewer_name=Dark2
stroke-opacity=0.7 ##SVG Transparency
fill-opacity=0.7 ##SVG transparency
stroke-width=0 ##SVG 相关属性
```



3.9 Pairwiselink diagram example

Example 1

The format is: [chr Start End Flag] where Plot_type = PairWiseLink

See example 09 OUT 1 in the figure below, you can see the distance of the pair end on the sca.

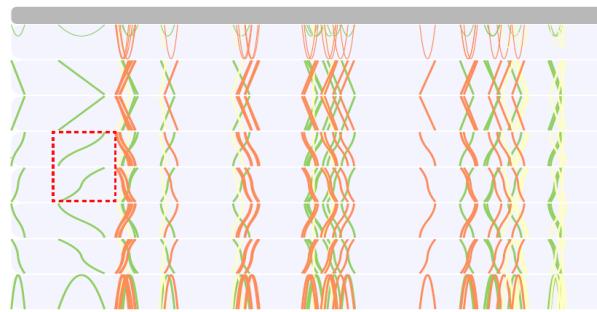
Among them

```
## link_uniform_height=1 # In PairWiseLink, this parameter can be as high when set to 1
## link_linestyle = curve # Default is curve or curve/line
## link_direction =UpUp ## In PairWiseLink, when this parameter is set to DownDown, the
radian down default is up UpUp This parameter can also be set to UpDownFor example, see
configuration 3 in the example. See also Say More Explanations
```

The following is a schematic diagram of the effect of different parameters of the same data:



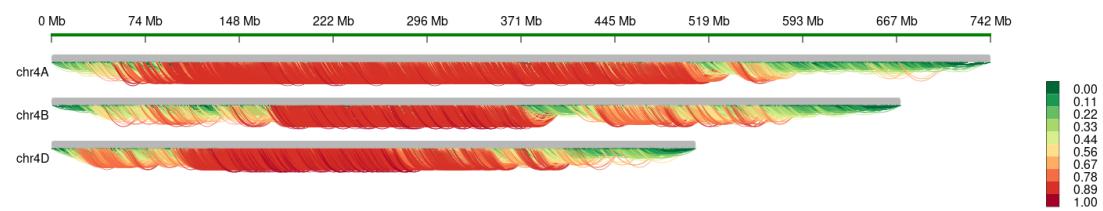
link_linestyle	link_direction	link_uniform_height
curve	UpUp	0
line	UpDown	-
line	DownUp	-
curve	DownUp	-
curve	DownUpV2	-
curve	UpDown	-
curve	UpDownV2	-
curve	DownDown	1



Example 2

Then take a SNP for every 1M in the R^2 figure as shown in the following figure to see the relationship between 30M-40M and its relationship R^2. See example9 OUT3

```
SetParaFor=track2 ##下面开始处理第 2 layer parameter processing
show_columns = File1:4 ##把file1 的第 4 列用 pairwiselink
plot_type= PairWiseLink
background_color="#FFFFFF" ##背景色为#FFFFFF 为白, that is, do not draw the color of the back
track_height=30
stroke-width=0.5 ##线条细点
upper_outlier_ratio=1 ## The top of valueX layer is the highest point color [0.95], and the rest are
divided into equal parts
```



As shown above, there are mainly two layers, the first layer only draws the back bar, and the second layer uses PairWiseLink for the back bar to be white (i.e. not drawn). The height of the second layer can be customized through configuration.

Example 3

The above design input is

Chr	Start	End	Value
-----	-------	-----	-------

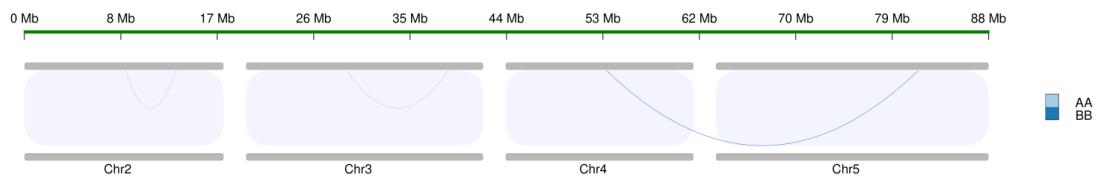


That is, from the start link of the same chr to End. The color or height is represented by the value of Value. ChrA StartA link ChrB StartB cannot be used, i.e. it cannot span two different chr. Therefore, PairWiseLinkV2 was developed . The PairWiseLinkV2 quasi-charge spans two different chrs, so it is also specified in the ShowColumn, and 3 columns must be specified at the same time, such as File1:4,5,6 # must be 3 columns, which can be different from FileX but must have three columns, namely Vale ChrB SiteB, and the other parameter link style is the same as above. Here's it

```
SetParaFor=track1 ##下面开始处理第 1 层的参数处理，第一层只有背景条
track_height=10
plot_type=EEE

SetParaFor=track2 ##第二层
plot_type= PairWiseLinkV2
background_color="#F4F4FF" ##背景色
track_height=100
stroke-width=0.5 ##线条细点
show_columns=File1:4,5,6 ##必须是 3 列分别为 Value ChrB SiteB
colormap_legend_show=1

SetParaFor=track3 ##第三层
plot_type= EEE
track_height=10
```



3.10 LinkS diagramming example

Example 1

The above pairwiselink is a starting point for a link to another starting point, but it cannot be inked to another area in one area, which is currently solved by LinkS. The input Chinese piece is

```
ChrA    StartA   EndA   Value chrB   StartB   EndB
```

To use it, you only need to have four lines of input in ShowColumn, if there are no four lines, you will not draw

That is, ShowColumn can be set to

ShowColumn=File2:4,5,6,7 or ShowColumn=File2:4 File2:5 File2:6 File2:7

The parameter label = "SampleA" can be set to the label of the current layer and its style settings (label_size label_color label_shift_x label_shift_y label_angle).

Among them *chr_order* the following settings, only part of chr is drawn, and Ch1H and Chr04H are not drawn

```
SetParaFor = global ##设置全局范围(global)
File1 = .. /Scene_Usage/example03_T2T_telo/chrlist.txt
File2 = SV.info
chr_orientation = horizontal ##染色体排列方向是水平的

chr_order = Chr2H, Chr3H, Chr5H, Chr6H, Chr7H ## 屏幕上显示的染色体顺序 (从左到右)。
track_num = 3 ##指定绘图层数 (number of tracks).
xaxis_tick_show=0
```



```

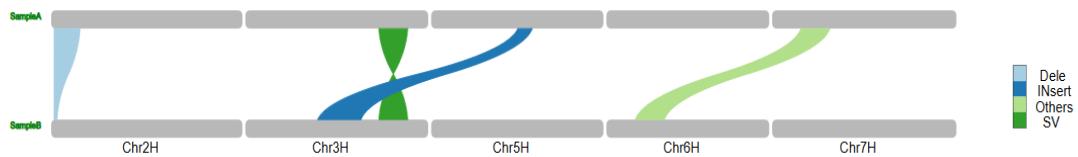
SetParaFor = track1
plot_type = linesEE ##不 painting, background bar only
show_columns = File1:4
label = "SampleA" ## The label of the current layer

SetParaFor = track2 ## Start processing layer 2 parameters
plot_type =LinkS
track_height = 100 ##当前层的高度 Raise it (i.e., track height).
show_columns = File2: 4,5,6,7 ##显示 linkS requires 4 columns, all of which are the same file File2
background_show=0 ## No background

SetParaFor = track3
plot_type = linesEE ##不 painting, background bar only
show_columns = File1:4 ##显示 Column 4 of File1
label = "SampleB" ## The label of the current layer and its styling (label_size label_color ....)

```

The effect is as follows:



3.11 HeatmapAnimated mapping example

Example 1

Here, heatmapAnimated dynamic heatmap refers to the change of heatmap color over time (state) in SVG files, which can dynamically display the distribution and changes of data at different time points (states). The main usage is ShowColumn=, just specify multiple columns, as follows:

```

SetParaFor= global
File1= ./S01.bin.gz
track_num = 2 ## How many layers, how many circles are the same as circos, here are 2 layers
canvas_margin_right=250 ## Extended dot on the right side of the canvas

SetParaFor= trackALL ##trackALL, which is the default value set for all layers first

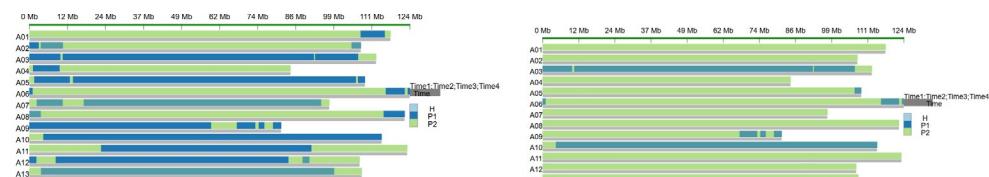
SetParaFor=track1
plot_type = heatmapAnimated ## Select the method of drawing as the dynamic heat
show_columns=File1:4,5,6,7 ## must be four columns in the same file
padding_ratio=0.1

SetParaFor=track2
plot_type= EEE ##不画 Background bar only
show_columns= File1:4
track_height=10 ##这一层 track width small dot

```

This function is rarely used, because it is dynamic, **you need to download the svg to the local area and open it with a browser to view.**

The above is shared into 4 columns, that is, 4 states, as shown in examp11

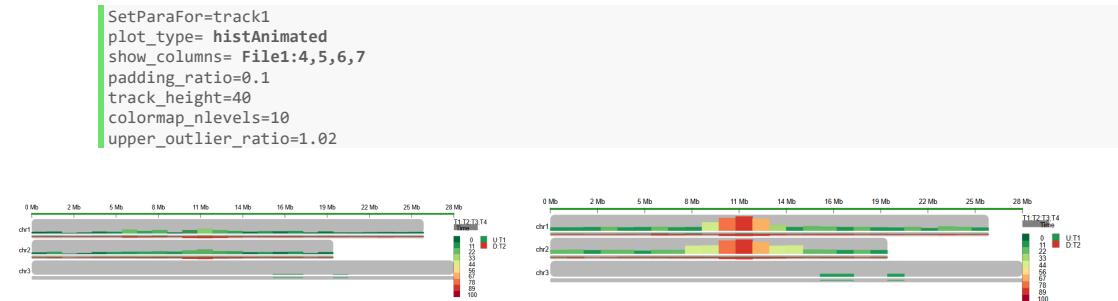


3.12 histAnimated drawing example

Example 1

As with heatmapAnimated, *ShowColumn=* specifies multiple columns, but heatmap has been changed to hist, see example 12. This function is rarely used, because it is dynamic, **you need to download the svg to the local area and open it with a browser to view.**

The above is shared into 4 columns, that is, 4 states, the following is a static diagram of the two shapes see examp12



4 Examples of application scenarios

4.1 SNP/gene/GC isodensity map

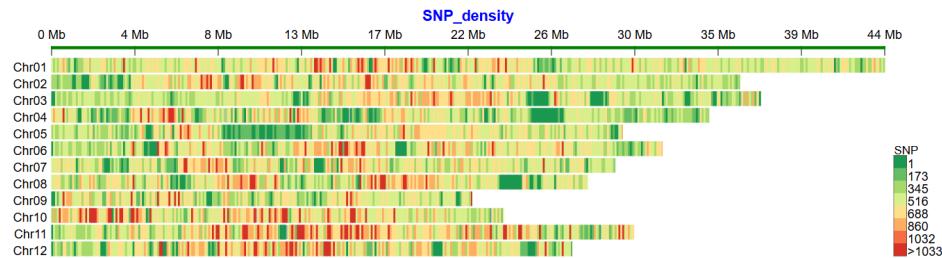
Input Format: [#Chr Stat End Flag]: Flag is the value of the statistic in this area, which can be an integer, a decimal, or a string. Among them, the figure below uses binboxThe size can be expressed by color.

In addition, users can draw the result data with poinhigh and low bar charts and lines and combined colors. **plot_type defaults to heatmap**,

Therefore, it can be configured minimally, just pass in the file

```
SetParaFor= global
File1= ./SNP.dis.gz
```

See Basic_Tutorials/example01 for specific configurations and data



In order to greatly facilitate the user and create diagrams, we provide a small perl script (CountBinNumPlot.pl) **in the corresponding directory example01_Density_heatmap**, which can be used from VCF to the above diagram in one step.

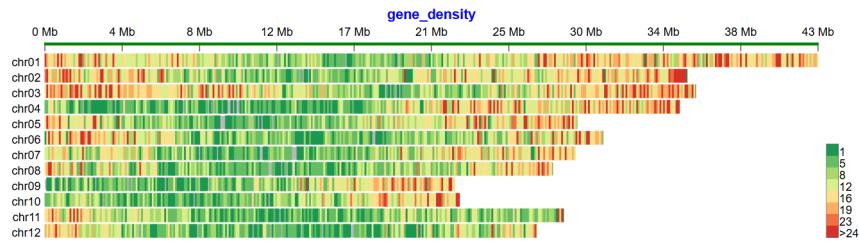
```
##### SNP/InDel density #####
perl CountBinNumPlot.pl -InFile in.vcf.gz -OutPut SNP_density
#perl CountBinNumPlot.pl -InFile in.vcf.gz -OutPut SNP_density -BinSize 100000
```



That is, the program has more parameters, not just for the VCF format, and can bin accumulate and average a column.

```
##### gene density #####
cat Ref.gff |awk '$3=="mRNA"' >mRNA.gff
perl CountBinNumPlot.pl -InFile mRNA.gff -SiteColumn 4 -OutPut gene_density
```

That is, the following gene density diagram can be obtained:

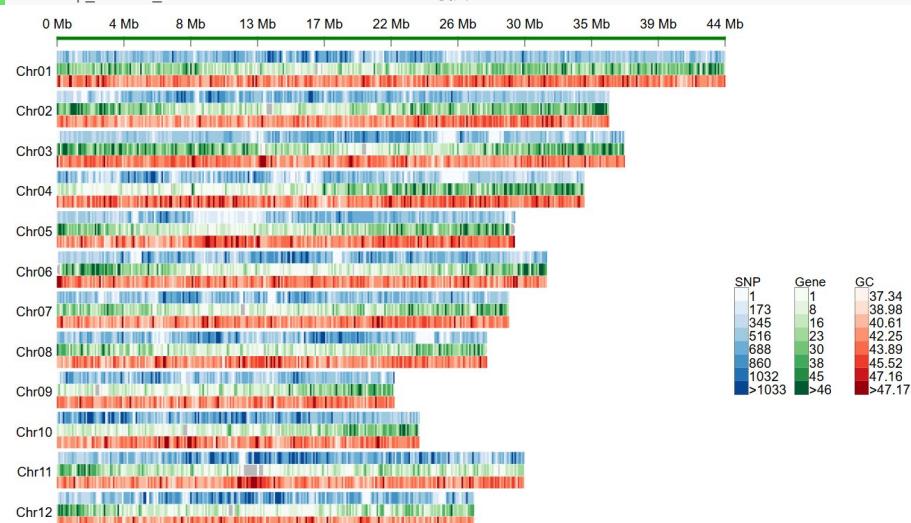


There may also be multiple tracks drawn together, and below are different color series for each track

```
SetParaFor=track1
show_columns=File1:4
colormap_brewer_name=Blues
##确定绘图中需要显示的列, the file is located
##使用 Tune Rcolorbrewer's Blues swatch

SetParaFor=track2
show_columns=File2:4
colormap_brewer_name=Greens
##确定绘图中需要显示的列, the file is located
##使用 Tune Rcolorbrewer's Greens swatch

SetParaFor=track3
show_columns=File3:4
colormap_brewer_name=Reds
##确定绘图中需要显示的列, the file is located
##使用 Tune Rcolorbrewer's Reds swatch
```



(By the way, the Chinese format is as follows: when you add one more #, the title will be added to the legend above).

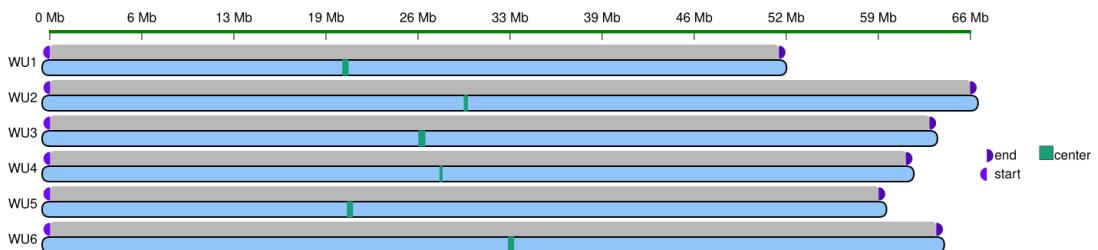
```
#Chr Start End #GC
Chr01 1 100000 44.39
```

4.2 T2T genome drawing

After stabilizing RectChr, according to the new needs of users, that is, the parameter `track_shift_y` that is only available in versions after 1.39, this parameter can mainly achieve the function of using **multiple graphing methods on the same track**

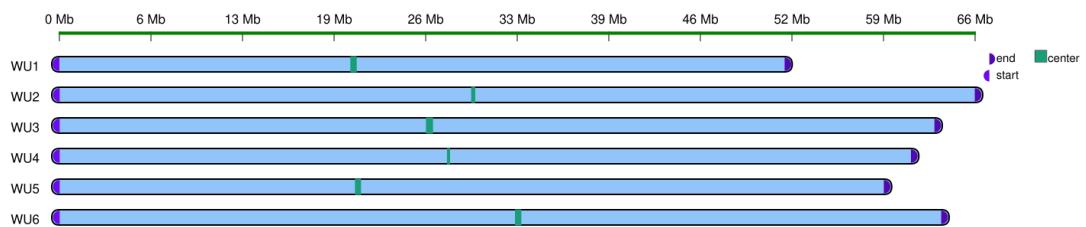
The details are as follows: 2 tracks were drawn, the upper one used shape and marked two telomeres with two semicircles, and the lower track used highlights to mark the centromeres



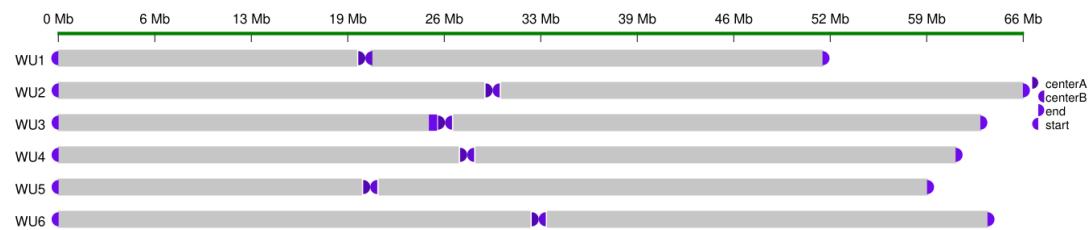


So how to draw two tracks together, in fact, as long as A: set the background of track1 to transparent, B: set the new parameter **track_shift_y=20** means to move track1 down from Y by 20, superimposed on track2, that is, just add the following parameters to track1

```
bg_stroke_width=0 ##不画此层的, cancel the background color
background_color="#FFFFFF" ##此 The background of the layer (track) is white, that is, it is not drawn
track_shift_y=20 ##track down and track2 stacked together
```



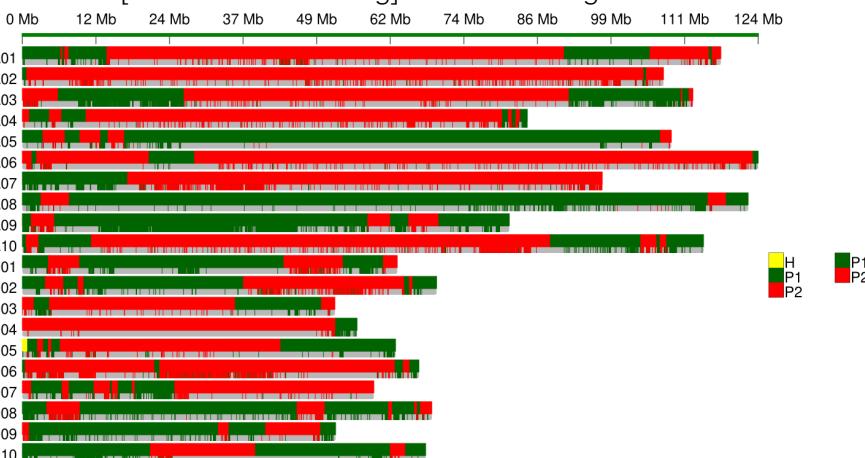
For more details, see `in2conf` and `in3conf`, see this figure below:



4.3 Individual BinMap+maker drawing

Input File 1 Format: [#Chr Stat End Flag] where the flag is: P1/P2/H

Input File 2 Format: [#chr site site Flag] where the flag is: P1/P2



See the configuration in example4

```
SetParaFor= global
File1= sample.bin2.gz ##File1 is a must enter parameter
```

```

track_num = 2 ##多少层， which is similar to how many circles circos

SetParaFor=track1 ##下面开始处理第 1 layer Parameter processing Color swap
colormap_low_color="#FFFF00"
colormap_mid_color="#006400" ##此层(ValueX) The color scheme of the middle value Value

SetParaFor=track2 ##下面开始处理第 2 layer parameter processing
File2= ./diff.spe.maker.gz ##可以输入别的文件 file1 is compatible with GZ
show_columns= File2:4 ##把 file2 的第 4 columns are drawn in the form of highlights
track_height=10 ## The width of this layer (track) becomes smaller
colormap_low_color="#006400"

```

Mainly two layers of heatmap, the next track is *smaller* *track_height=10*. That is, you can get the above figure, which can see which of the offspring is from which parent.

4.4 Multi-region multi-sample population BinMap

The above is a sample to see which parent it comes from, and the common breeding group (such as the RIL group) will test many individuals, if you want to draw it together, then this picture is very simple to use heatmap to draw multiple layers, as many samples as there are layers, and the gap between each layer is set to 0; At the same time, each chr is released horizontally.

- A. Draw the information of a sample into a layer, that is, as many samples as there are (*track_num =79*) The gap comparison of each layer is set to 0 (*padding_ratio=0*).
- B. Samples are arranged in different subgroups, with several random samples inserted between the different subgroups for separation.
- C. chr horizontal (*chr_orientation=horizontal*), small gap point (*chr_spacing_ratio=0.1*).
- D. The last column is color, you can customize the color or default

See example 9 for specific configuration files and examples

```

SetParaFor= global
File1= ./data/S01.bin.gz
track_num = 79 ##79 samples, one track per sample, i.e. 79 layers
chr_spacing_ratio=0.1 ##不同染色体 chr 之间的间隔比例
colormap_conf = cor.info ##通过在主配置文件 input Custom color and Value correspondence
chr_orientation = horizontal ##chr是按纵 horizontal 横排列

#canvas_height_ratio= 0.7

SetParaFor= trackALL ##下面为 trackALL, which is the default value set for all layers first
plot_type= heatmap
track_height=10 ##79*10 Approximate canvas depth is 790+
colormap_legend_show=0 ##不显示进度条
chr_label_size_ratio=1.05          ##chrName 放大 1.05 times
show_columns= File1:4

#colormap_legend_shift_y=-550
#colormap_legend_shift_x=20
colormap_legend_size=1.25

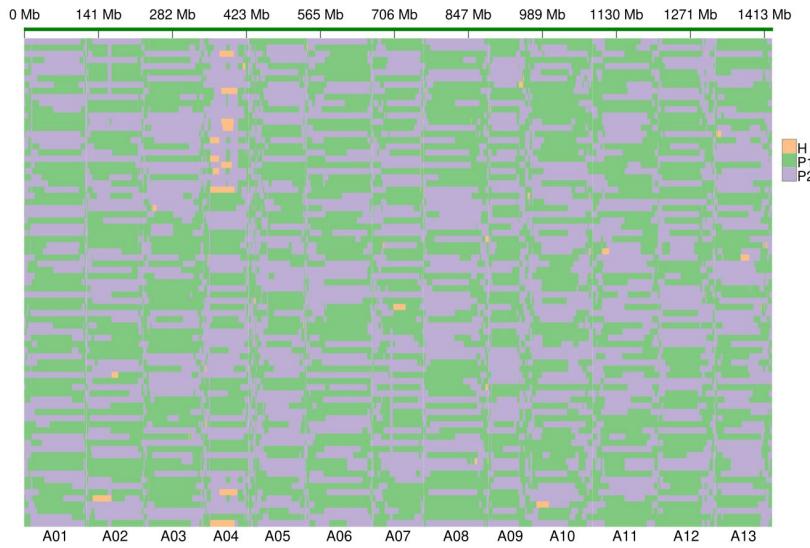
SetParaFor=track2
File2= ./data/S02.bin.gz
show_columns= File2:4
SetParaFor=track3
File3= ./data/S03.bin.gz
show_columns= File3:4

#####在这省略 5-77 layer setting #####

```

##See example04_RILBinMap for details and provide specific data and scripts





4.5 Single-region multi-sample population RegionHaplotype

Population resequencing In the analysis, a region is selected through some information, depending on all the samples (by different subgroups) to see this regionHaplotype. The distribution law often needs to be carried out on a certain area Haplotype display.

`/bin/script/GenotypeShow.pl` is provided, which reads the vcf file directly, generates the relevant format and calls RectChr to plot the image, and the usage is as follows:

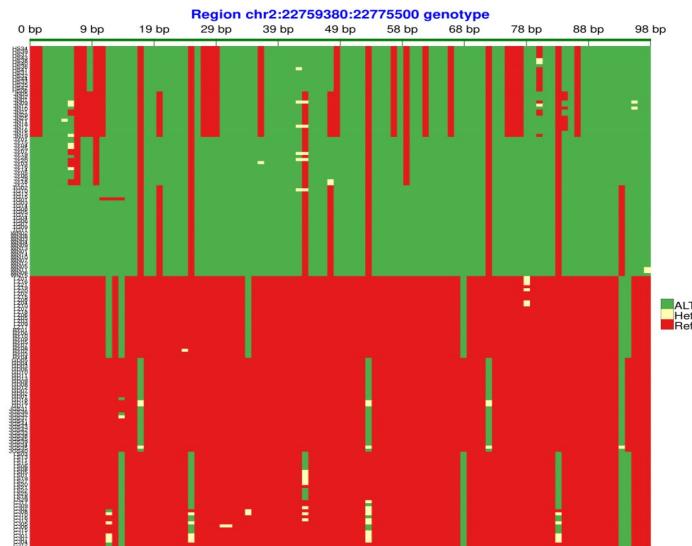
```
perl GenotypeShow.pl
Version 1.0      hewm2008      2021-06-28;
Usage: GenotypeShow.pl <InPut><chr:start:end><Out>
Usage: GenotypeShow.pl <InPut><chr:start:end><Sub_or_OrderSample><Out>
```

Enter the in.vcf and the corresponding area interval.

There is also an additional parameter that can be used to sort the sample or extract only the parameters Sub_or_OrderSample of the subgroup as a file, which is a column and the first column stores the sample name

```
perl .. /bin/script/GenotypeShow.pl    in.vcf.gz    chr2:22759380:22775500    sample.order.list OutRegion
#perl .. /bin/script/GenotypeShow.pl    in.vcf.gz    chr2:22759380:22775500    OutRegion
```

That is, you can get the following:



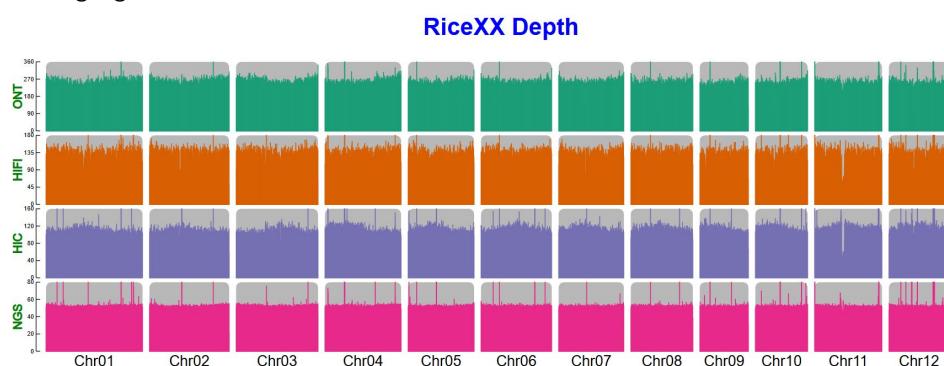
The calling principle is to treat the information of a sample as a chr, and the gap comparison between chrs is set to 0 when arranged vertically example05_RegionHaplotype. For more details, click here to view [the genotype/gene/haplotype heat map of a region of multiple samples of RectChr](#)

4.6 Assembly Depth Coverage Diagram

Sometimes a genome is assembled, and the diagram needs to be assembled to see the assembly effect and explain the yield, and the depth of various data of the genome must be drawn, at this time, chr is arranged vertically, and all kinds of data are a track, with a column plot, but this situation often exists, because multiple CNVs only assemble a copy, which will cause the depth of this area to be extremely high, which is the extreme value, these parameters **cap_max_value(cap_min_value)** is the maximum (minimum) **truncation value of the track's data**, that is, when it is higher than this value, this value is taken. For more information on the example track1 below, see example06_DepthCov table of contents

```
SetParaFor=track1
show_columns= File1:4
colormap_low_color="#1B9E77"
colormap_mid_color="#1B9E77"
colormap_high_color="#1B9E77"
label= "ONT"
cap_max_value=360
#Ymax=360
#bg_end_arc_division=98
```

The following figure can be obtained:



4.7 Genetic statistics and other joint plots

In this section, it is mainly explained that each track can be freely combined, as shown below example07_Genetics The following three layers

A: Use line to indicate line: Pi

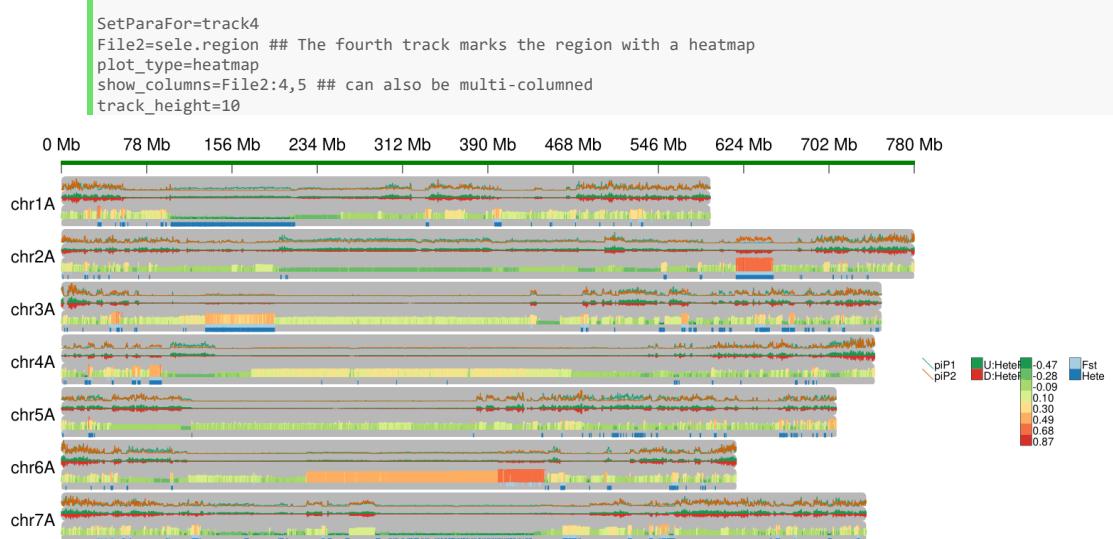
B-pillar + color indication: heterozygous

C Fst uses the heat map for the hist sele region

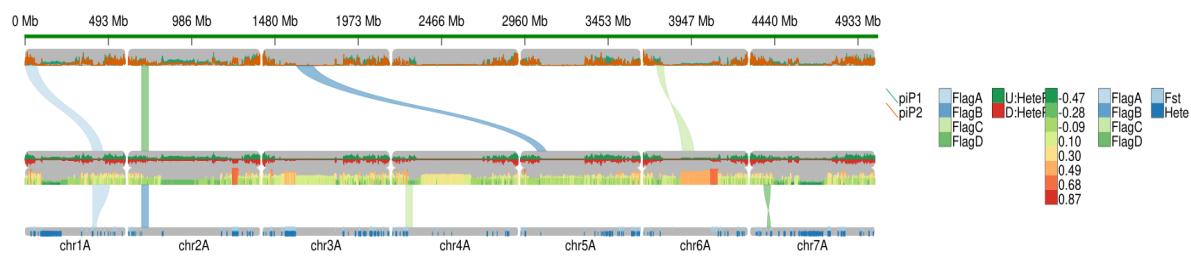
```
SetParaFor=track1
plot_type = lines ## The first track uses lines
show_columns= File1:4,5 ##把file1的第4,5列在形式上画成两条线图

SetParaFor=track2
plot_type = histogram ## The second track uses lines
show_columns = File1:6,7 ##把file1的第6,7列在形式上画成上下两行

SetParaFor=track3
plot_type = histogram ## The third track uses columns + colors
show_columns= File1:8
```



Among them, LinkS is combined with each other, that is, LinkS is added and horizontal is shown in in2.conf. The result graph is as follows



4.8 Manhattan diagram of GWAS with a sense of luxury

When I introduced [scatter \(point\) above](#), the display results of ordinary GWAS were already shown. Sometimes to mark some genes on peaks, add text, etc., we need a variety of track results, you can add 2 more tracks on top of the previous one, the first is text, and the second is **pairwiselink**

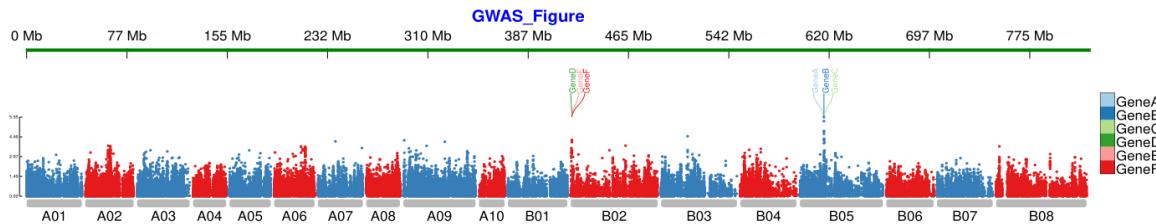
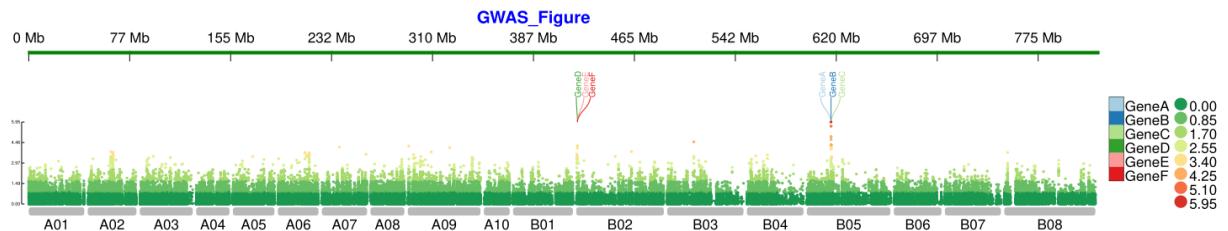
```

SetParaFor=track1 ##下面开始处理第1层 parameter processing
plot_type= text
show_columns = File2:5 ## Column 5 of File File2 is plotted
background_color="#FFFFFF" ##白色, that is, no background is drawn
track_height=40 ##放text的名字, so the width is longer
#track_text_angle=-90 ##Text rotation 90 degrees
track_text_size=1.2 ## The text font is enlarged to the original 12
colormap_legend_show=0 ##不显示渐变条 Column

SetParaFor=track2
show_columns = File2:5 ##把file2的第5 columns with the ParrWiseLink S curve
track_height=30 ##这一层宽度调高点
plot_type = PairWiseLink ## Bézier curve
link_direction= UpDown
background_show=0 ## is the same as background_color="#FFFFFF", that is, there is no background
colormap_legend_size=0.8 ##渐变条 Reduced to the original 0.8

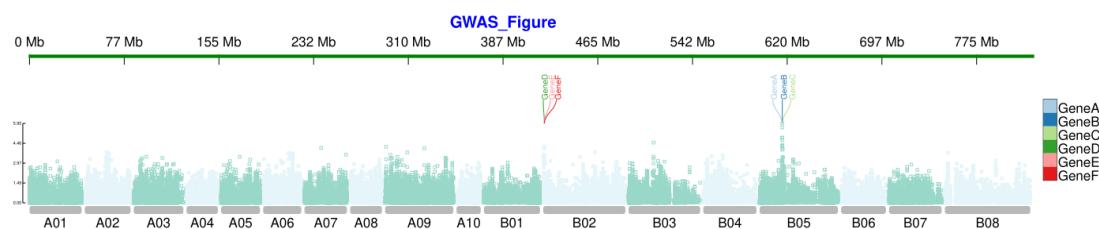
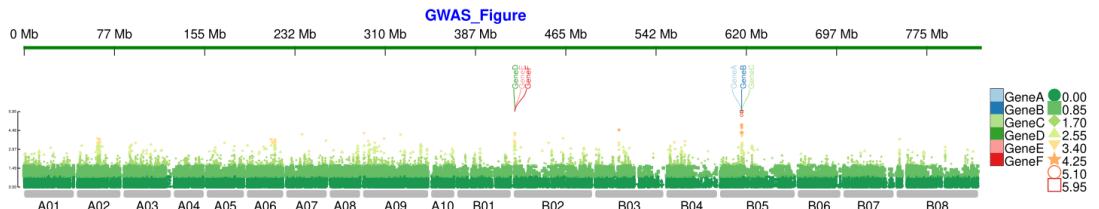
```





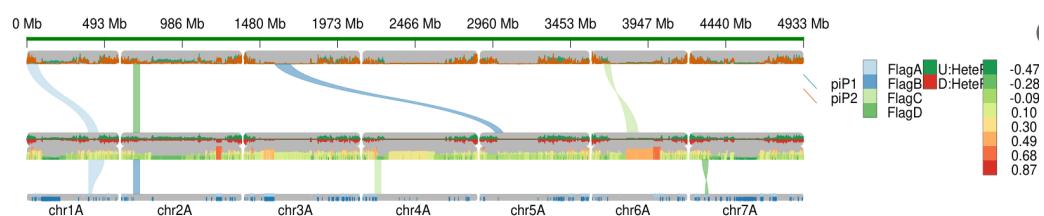
See also the `run3.sh` inside to change the dot diagram to shape.

For the specific shape parameters, see below or [open this to see the instructions](#)



4.9 Local amplification function (zoom_region) genome local

In the previous version, the `chr_order` under `SetParaFor = global` was mainly used to sort the order of chr and list only one or several chr, but there was no way to display only a specific area, now just add `zoom_region` to `SetParaFor = global` (*the same as chr_zoom_region*), followed by a specific area, such as ChrA:StartA:EndA

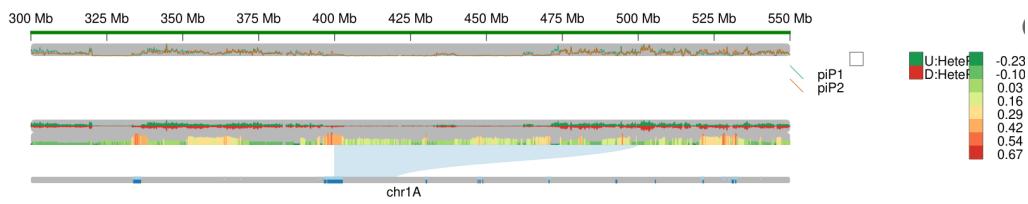


As in the application context [Example 5.7](#) in `2.conf`, Add the following

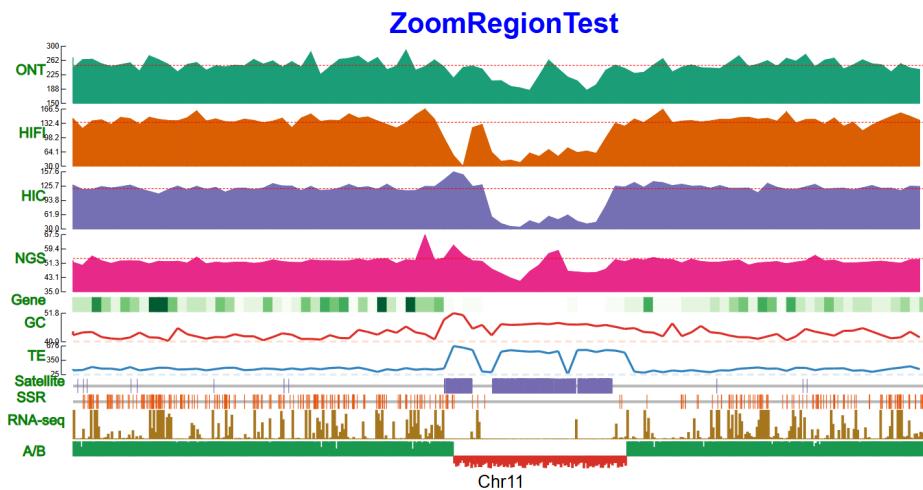
parameters

```
zoom_region=chr1A:300000000:550000000 #即可以只放大这个区域的情况。
```

You can get the following figure: You can see that the coordinates are only shown from 300M-550M

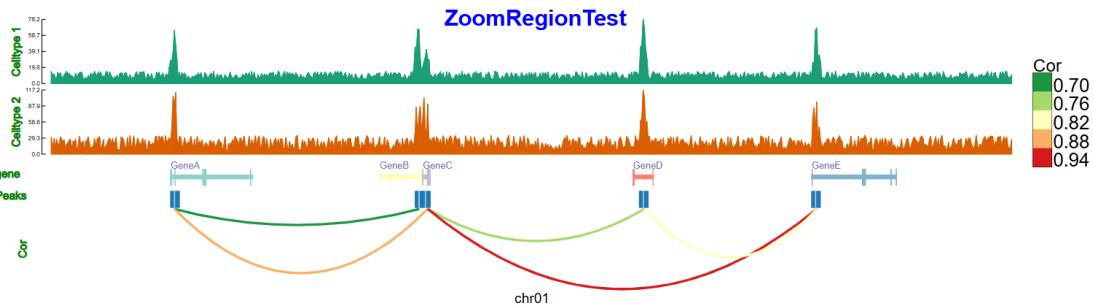


In example09_ZoomRegion, we show the following diagram that can be used for the article (centromeres in the middle):



The above figure shows the *local situation at zoom_region=Chr11:8000000:17000000*.

Example 10_Peak shows the gene structure and relationships of a specific region, as shown in the figure below.



5. Other settings explanation

5.1 RectChr color details

A: RectChr early colors were mainly made up of three colors (starting with the middle and outcome) (`colormap_low_color` `colormap_mid_color` `colormap_high_color`) and equal fractions (`colormap_nlevels`).) to assign colors

```
#colormap_nlevels=3
#colormap_low_color = "#006400" ## The color corresponding to the lowest value
#colormap_mid_color = "#FFFF00" ## The color corresponding to the middle value
```



```
#colormap_high_color = "#FF0000" ## The color corresponding to the highest value
```

B: But in the later stage, there are many colors of the layout artboard. Two parameters are provided at each layer **colormap_brewer_name** and **a function of colormap_reverse**. It also retains the function of the previous three-color gradient.

If you set **colormap_brewer_name** the three-color gradient will not work.

If you don't have **a colormap_brewer_name**, start the previous color only when you set the Tricolor Gradient (**colormap_low_color colormap_mid_color colormap_high_color**).

B.1 The panel has RColorBrewer's built-in panel, and its homepage is here:[R Color Brewer's palettesR](#)

RColorBrewer A visual URL is also provided:[Color Advice for Maps](#)

The words of Guan Jian are as follows, and the corresponding color bars are as follows:

```
"BrBG","PiYG","PRGn","PuOr","RdBu","RdGy","RdYlBu","RdYlGn","Spectral"  
"Accent","Dark2","Paired","Pastel1","Pastel2","Set1","Set2","Set3"  
"Blues","BuGn","BuPu","GnBu","Greens","Greys","Oranges","OrRd","PuBu","PuBuGn","PuRd","Purples","RdPu","Re  
ds","YlGn","YlGnBu","YlOrBr","YlOrRd"  
"BrBG","PiYG","PRGn","PuOr","RdBu","RdYlBu","Dark2","Paired","Set2", # GnYlRd greenishyellow-red by  
default
```



B.2 where **the above colormap_brewer_name=xx**, before 1.42, xx could only be

Rcolorbrewer's name (Set3 Dark2 ... Now, just put a file (such as bs5) in the ColorsBrewer directory of the program, and then **colormap_brewer_name=bs5** (i.e. can customize the color panel). BS5 is formatted as follows. The ggsci-related color scheme has now been processed in the ColorsBrewer catalog.

```
NewParaList.xlsx Scene_Usage  
(base) 1iaojing@node1:/home/liaojing/07.tmp/RectChr-1.42  
$ ls ColorsBrewer/  
aaas d3 gsea locuszoom primer tron  
atlassian flatui igv material rickandmorty tw3  
bmj frontiers jama nejm simpsons uchica  
bs5 futurama jco npg startrek ucscgb  
cosmic get_colors.pl lancet observable tmp  
(base) 1iaojing@node1:/home/liaojing/07.tmp/RectChr-1.42  
$ head ColorsBrewer/bs5  
#f8f9fa  
#e9ecf  
#dee2e6  
#ced4da  
#adb5bd  
#6c757d
```

在 1.42里面会多一个ColorsBrewer 的目录
里面可以自定义放颜色面板
如bs5 文件里面格式如下



C: The mapping of value to color is automatically sorted by value or ASCII code (can also be manually specified) and **divided into equal** parts (can limit the maximum, smallest, minimum value and other related parameters) to color. Users can also customize the color **mapping file path via colormap_conf = col.file ##** to specify the value to color mapping relationship, i.e. custom color. The format is as follows:

```
Value1=red
Value2="#f8f9fa"
...

```

5.2 RectChr legend legend arrangement

Versions after 1.41 have an additional parameter colormap_legend_layout, the default value is 1, a total of 14 options can be 0-13, and the canvas will automatically change according to the number of legends. The corresponding arrangement is as follows:

value	Illustration	value	Illustration	value	Illustration
0		1 Default		2	
3		4		5	
6		7		8	
9		10		11	
12		13		Others	Same as 0 do not draw legend

Also added that colormap_gradient_gap is the gap between the front and back legends
The parameter colormap_legend_gap is the gap between the two flags above and below the same legend.

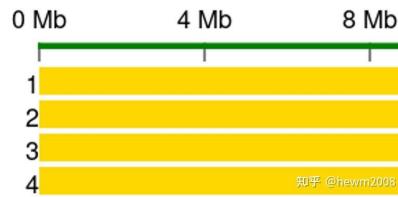
Other related legend parameters can also be used: colormap_legend_show/
colormap_legend_shift_x/colormap_legend_shift_y/colormap_legend_size

5.3 Detailed explanation of the chr edge curvature of RectChr

RectChr is by default multi-equal edge, i.e. micro-radian. Roughly as shown below



Under the corresponding layer `bg_end_arc=0` This was canceled immediatelyRadians, becomes as follows:



However, at this time, some people asked how to achieve a large arc. As follows

In fact, it can be adjusted, the default third-equal edge above is actually changed to biparte, that is, a semicircle, using the hidden parameter `bg_end_arc_division =2`(the minimum value can only be 2, the maximum value is `bg_end_arc =0`) as follows



However, when the user compares the above, when it is at 10bp, draw a vertical line and find that it breaks through this semicircle. As shown below

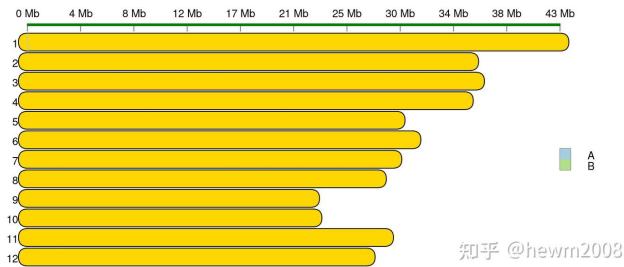


After comparison, it was found that the sample diagram was actually not included in the coordinate system. New hidden parameters were added in 1.30 upon request `bg_end_offset =1` When the time comes, you can draw this semicircle in coordinate systemOutside the body, so that it will not be pierced. Among them `bg_end_offset =1` It only works when the chr is firmly aligned.



bg_end_arc_division =2 at the same time bg_end_offset=1

Well, this time add ***bg_stroke_width =2*** to the width of the background link and the color of the back edge ***bg_stroke_color=black*** to get the following



5.4 RectChr's X-axis Detailed discussion

Parameters related to the X axis:

```
#xaxis_tick_show=1          ## bool 0-1      Whether the X-axis is displayed
#yaxis_tick_show=0          ## bool 0-1      Y-axis display

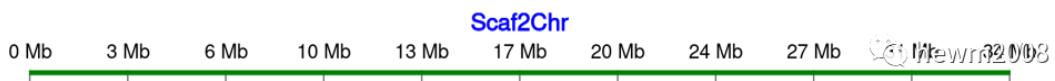
#axis_tick_unit             ## text, for customization such as kb bp cm mb Coordinate axis scale
unit, automatic judgment
#axis_text_angle=0           ## Integer (-360,360) Axis text angle

#axis_tick_num=10            ## Integer Number of coordinate axis scales
#axis_tick_interval          ## Integer The coordinate axis scale interval, such as an interval of
every 10M, will be invalid if it is started axis_tick_num
#axis_tick_precision         ## Integer Coordinate axis scale accuracy, automatic judgment
#xaxis_shift_y               ## Numerical values X-axis vertical offset
```

Cancel the coordinate system, there is a parameter of equal coordinates under global (default 10), and change this one to minus 1 [***axis_tick_num =-1***] or ***xaxis_tick_show=0*** can cancel the coordinate axis.

If MaxChr length 111M is 10 points, it is 0 11 22 : Can you customize the 20 M (custom gradient) and add ***axis_tick_interval*** parameters under global, that is, add ***axis_tick_interval =20000000 under global*** (*plus axis_text_angle=*). Rotation can also be used, hiding parameters).

The default coordinate system is the result of 10 equal parts according to the longest chr length of 34M as follows:



If you add ***axis_tick_interval=5000000*** to global, it becomes as follows:

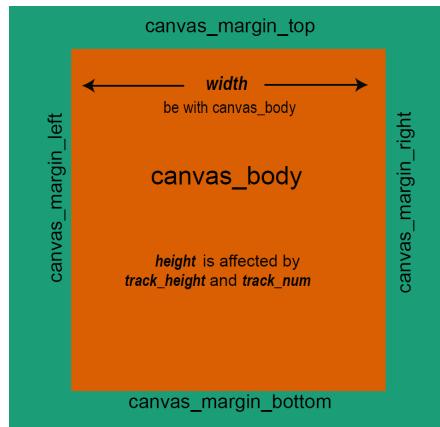


5.5 RectChr Canvas Settings

The relevant parameters of the canvas are here:

```
#canvas_body = 1200 ## Main canvas size, default is 1200
#canvas_margin_top = 55 ## Canvas margin, default to 55
#canvas_margin_bottom = 55 ## Canvas bottom margin, default to 25
#canvas_margin_left = 100 ## Canvas left margin, default to 100
#canvas_margin_right = 120 ## Canvas right margin, default to 120
#canvas_width_ratio=1.0 ## The scale of the canvas width
```

```
#canvas_height_ratio=1.0          ## Scaling of the canvas height
```



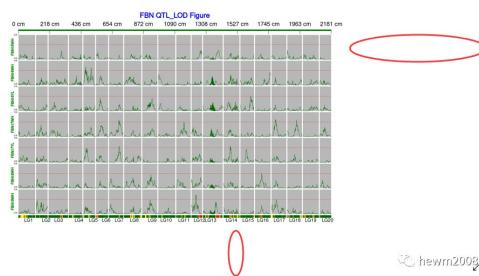
Sometimes the name of the chr on the left is too long, so it is not possible to display the full chr, as shown below



You can make ***the canvas_margin_left*** bigger to solve it

```
# canvas_height_ratio =1.0 and # canvas_width_ratio =1.0
```

In fact, it is understandable to cut off the blank space below and the blank space on the right.



When in multiple layers `colormap_legend_show=0` is the legend of each layer when it is not displayed, in which case there is often a large blank space on the right (**Versions after 1.41 will no longer be left blank**)。 As shown below, there are 8 floors in total, and each floor has been canceled Gradient strip, so the canvas has a lot of white space on the far right and left. So add two more lines under global

```
canvas_height_ratio =0.8  
canvas_width_ratio =0.7
```

That is, the base height is reduced to the original 0.8; Width is the original 0.7;

Of course, a small part of the legend is blocked when drawing, as long as the corresponding two parameters are greater than 1;



6. Download and install

6.1 Download URL

Continuous updates are here: [Remember to add a star when](#) downloading
<https://github.com/hewm2008/RectChr>

6.2 Pre-Installation

RectChr is available for Linux/Unix/macOS systems. Before installing, install the following conditions of use:

- 1) Perl: Within Perl[Module SVG.pm](#) (<https://metacpan.org/release/SVG>) . Can be pre-installed. Although we already have SVG built into the installation package.pm packaged
- 2) [convert](#): system command to convert svg to png. It doesn't matter if there is none, it is better if there is

6.3 Installation

Users can run it with the following direct chmod 755 (linux/MacOS):

```
git clone https://github.com/hewm2008/RectChr
cd RectChr ; chmod 755 -R bin/*
./bin/RectChr -h # directly run
```



7. Usage and parameter description

7.1 RectChr Parameters

The program RectChr is simple, one input and one output. The details are as follows.

```
[heweiming@cngb-ologin-25 bin]$ ./bin/RectChr
Version:1.42          hewm2008@gmail.com

Options

-InConf      <s> : Input Configuration File
-OutPut      <s> : OutPut svg file result

-help        : Show more help with more parameter
```

-InConf Input File The configured file
-OutPut output file, out.svg

-help See configuration parameters for details

The program will perform a simple detection of the input configuration file, and if the abnormal configuration such as the file format and the number of lines do not match, it will report an abnormality, please check. Modifications can be made according to the prompts.

7.1.1 Main configuration parameters

SetParaFor is the setting parameter, can be a global variable for global, ALL is a parameter for all layers, trackX is a parameter for layer X

The main parameters of the configuration file are explained as follows

Serial number	Example	Interpretation Description
Parameter 1	FileN = /path/in.data	(N=1,2,3...) The path to the Nth file is entered
Parameter 2	Plot_type = heatmap	[One of Guan Jian's words: heatmap/ highlights/LinkS/ pairwiselink/ histogram/hist/ scatter/ point/shape/text/line/lines/heatmapAnimated and histAnimated, that is, there are 13 drawing methods] If it is not a strong word, it is not drawn, only the background bar (See the previous for details of each drawing method) Example of drawing method



Parameter 3	show_columns = File1:8 File2:5,6	Column X of a file is used as a statistic

Some other important parameters are shown in the screenshot below,

参数级别	参数	重要性	字样	简说明	详说明
track	colormap_low_color	**	文本, 颜色	渐变起始颜色	确定绘图中渐变效果的起始颜色
track	track_geom_shape	**	整数 (0-13)	形状类型	确定绘图中所使用形状的类型, 如圆形、方形等
track	link_direction	**	文本, 特定字符	上下样式	定义绘图中元素上下部分的样式
track	link_linestyle	**	文本, 特定字符	线条类型	定义绘图中线条的类型, 如实线、虚线等
track	chr_scale_ratio	***	浮点, 比例, 可大于1	染色体长度比例	控制染色体长度相对于某个基准长度的比例值
global	title	***	文本	主题文本内容	定义绘图主题的文字内容, 如标题等
track	log_p	***	bool 0-1	对数 P 值	可能用于处理以对数形式表示的 P 值
track	cap_max_value	***	数值	上限值	设定一个上限值, 用于限制数据的显示范围
track	cap_min_value	***	数值	下限值	设定一个下限值, 用于限制数据的显示范围
track	Ymin	***	数值	最小值	确定绘图数据中的最小值
track	Ymax	***	数值	最大值	确定绘图数据中的最大值
track	padding_ratio	***	浮点, 比例, 可大于1	面板分隔比例	控制面板之间的分隔距离, 以比例形式表示
track	track_height	***	整数	面板高度	设定绘图中面板的高度
track	label	***	文本	面板名称	定义绘图中各个面板的名称
global	colormap_conf	***	文本, 文件路径	颜色配置	对绘图中涉及的各种颜色进行统一配置, 如线条颜色、填充颜色等
global	chr_order	****	文本: chr01,chr02...	染色体顺序	规定染色体在画布上的显示顺序
track	chr_order	****	文本: chr01,chr02...	染色体顺序	规定在该级别下染色体的显示顺序
global	chr_zoom_region	****	文本, 文件路径	染色体区域缩放	对染色体特定区域进行缩放操作, 以便于更清晰地查看细节
track	colormap_brewer_name	****	文本, 特定字符	布鲁尔调色板	提供一组预定义的颜色组合, 用于绘图中的颜色配置
track	colormap_levels	****	整数	图例渐变数量	确定图例中渐变的数量
global	chr_orientation	*****	特定字符 水平或纵向	染色体排列方向	确定染色体在画布上的排列方向, 如水平或垂直排列等
track	plot_type	*****	文本, 特定字符	P 值类型	定义 P 值的类型, 如不同的统计检验得到的 P 值类型
track	show_columns	*****	文本, 特定字符, 如File	显示列	确定绘图中需要显示的列
global	track_num	*****	整数	面板数量	确定绘图中面板的数量

7.1.2 Other configuration parameters

Open all relevant parameters, many of which are default, but can also be listed

For more parameters, see Excel details

chr_label_shift_x	chr_label_shift_x	整数	染色体名称水平偏移量	调整染色体名称文本在水平方向上的位置
chr_label_shift_y	chr_label_shift_y	整数	染色体名称垂直偏移量	调整染色体名称文本在垂直方向上的位置
reverse_chr_order	chr_order_reverse	bool, 有则反	将染色体顺序	将染色体的显示顺序进行反转
axis_tick_unit	axis_tick_unit	文本, 为了自定义如kb bp cm	坐标轴刻度单位	设置坐标轴上刻度的单位, 用于确定刻度值的间隔
axis_tick_show	axis_tick_show	整数 (360,360)	坐标轴文本角度	调整坐标轴上文本的角度, 使文本显示更加清晰或符合特定需求
axis_tick_break	axis_tick_num	整数	坐标轴刻度数量	确定坐标轴上刻度的数据
axis_shift_y	axis_tick_interval	数值	坐标轴刻度间隔	规定坐标轴上相邻刻度之间的数值间隔
axis_tick_show	axis_tick_show	数值	X 轴垂直偏移量	调整 X 坐标轴文本垂直方向上的位置
title_color	title_color	整数	坐标轴刻度精度	确定坐标轴刻度值的精度, 即小数点后的位数等
title_size	title_size	浮点, 比例, 可大于1	Y 轴显示	控制 Y 轴是否在绘图中显示
title_shift_x	title_shift_x	整数	主题文本颜色	确定绘图主题文本的颜色
title_shift_y	title_shift_y	整数	主题文本大小	控制绘图主题元素的大小, 以比例形式呈现, 影响主题元素在图表中的显示位置
这个参数不对外公开 内置的	这个参数不对外公开 内置的	不理会	主题文本偏移量	控制绘图主题元素在水平方向上的偏移位置
as_flag	upper_outlier_ratio	浮点, 比例[0-1]	主题文本偏移量	控制绘图主题元素在垂直方向上的偏移位置
upper_outlier_ratio	lower_outlier_ratio	浮点, 比例[0-1]	上异常值比例	可能用于判断某个元素或数据是否为数字类型
rack_bg_height_ratio	track_bg_height_ratio	浮点, 比例	下异常值比例	可能作为一个标识, 用于特定的逻辑判断或状态指示
rack_background_color	background_color	文本, 颜色	用于处理数据中高于某个阈值的异常值的比例	用于处理数据中低于某个阈值的异常值的比例
rack_background_show	background_show	bool 0-1	背景显示	控制背景是否在绘图中显示
rack_end_arc	bg_end_arc	bool 0-1	背景染色体末端曲线	用于设置背景染色体末端的曲线形状
rack_end_offset	bg_end_offset	bool 0-1	末端曲线外扩	控制染色体末端曲线向外扩展的程度
rack_end_arc_division	bg_end_arc_division	整数	末端曲线弧度	設定染色体末端曲线的弧度大小
rack_bg_height_ratio	track_bg_height_ratio	整数	背景高度比例	确定背景部分高度相对于某个基准高度的比例值
rack_label_color	label_color	文本, 颜色	面板名称颜色	确定面板名称文本的颜色
rack_label_size	label_size	文本, 颜色	面板名称大小比例	调整面板名称文本的大小, 以比例形式表示
rack_label_angle	label_angle	文本, 颜色	面板名称角度	设定面板名称文本的角度
rack_label_shift_x	label_shift_x	整数	面板名称水平偏移量	调整面板名称文本在水平方向上的位置
rack_label_shift_y	label_shift_y	整数	面板名称垂直偏移量	调整面板名称文本在垂直方向上的位置
rack_colormap_reverse	colormap_reverse	bool, 有则反	反转布鲁尔调色板	对布鲁尔调色板中的颜色顺序进行反转
rack_colormap_mid_color	colormap_mid_color	文本, 颜色	渐变中间颜色	为绘图中渐变效果指定中间的颜色
rack_colormap_high_color	colormap_high_color	文本, 颜色	渐变结束颜色	确定绘图中渐变效果的结束颜色
rack_colormap_legend_show	colormap_legend_show	bool 0-1	图例渐变显示	决定图例中的渐变效果是否显示



`SetParaFor =X` is a flag parameter that sets each layer (X) and `global` is a global variable

`ALL` is a parameter that can be used by all layers, and if each layer is not configured, it will default to the global (`ALL`) parameter. The X layer, quite the X circle of cir cos

Here is an example: You can see the analysis of ## below

There are also more parameters available, but they are not commonly used, so they are hidden, such as the up and down movement of the X-axis coordinate system

`global : xaxis_shift_y =0`, etc. If more parameters are needed, you can give feedback~ Random addition and subtraction parameters are taken into account when programming.

```
#####
##### Global parameters #####
#####

SetParaFor = global ## Sets the current paragraph scope to global, which applies to the entire graph configuration

File1 = ./InPut.file ## Master data file path,
#File2 = ## Optional second data file path for multi-source data overlay FileX = ./InPut.fileX

#track_num = ## Specify the number of layers (number of tracks), which will be automatically inferred based on the number of columns in File1 by default (e.g., Value1 to ValueN).
#chr_spacing_ratio = 0.2 ## Ratio of intervals between different chromosomes, calculated based on track height (track_height * chr_spacing_ratio)
#title = "main_Figure" ## Graphic title and its styling settings, supporting parameters such as title_color, title_size, title_shift_x, title_shift_y, etc
#colormap_conf = col.file ## Custom color mapping file path to specify the mapping relationship from value to color (e.g. P1 = "#FE0808")
#chr_orientation = horizontal ## Chromosome alignment direction, optionally horizontal or vertical
#bg_end_arc = 1 ## Less used parameter to control special effects like background arcs

#####
##### global. Chromosomal parameter configuration #####
#####

#zoom_region = ## Scale a specific area in the format chr:start:end (e.g. chr2:1000:5000)
#chr_order = ## Specify the order of chromosomes or filter the list of chromosomes displayed (if not specified, automatically sort by name)
#chr_spacing_ratio = 0.2 ## The ratio of intervals between different chromosomes
#chr_label_rotation = 0 ## The angle of rotation of the chromosome label text

#####
##### global.canvas and image parameter configuration #####
#####

#canvas_body = 1200 ##主画布大小, the default value is 1200
#canvas_margin_top = 55 ##画布上边距, defaults to 55
#canvas_margin_bottom = 25 ##画布下边距, which defaults to 25
#canvas_margin_left = 100 ##画布左边距, default to 100
#canvas_margin_right = 120 ##画布右边距, the default is 120
#canvas_angle = 0 ##整个图形旋转角度 in degrees
#canvas_height_ratio=1.0 ##收缩放画布的整体高度
#canvas_width_ratio=1.0 ##收缩放画布的整体宽度

#####
##### ALL default configuration parameters for each layer If each layer does not have a configuration, the parameters here will be used #####
#####

SetParaFor = trackALL ## sets the default parameters for all tracks, which are inherited by subsequent trackXs that are not configured separately
plot_type = heatmap ## Supported plot types are: heatmap, lineand 13 other kinds,Check it out here
#show_columns = ## Specify the columns to display, such as File1:4 or File2:4,5
#colormap_brewer_name = ## Use a preset Rcolorbrewer palette such as GnYlRd (numeric) or Paired (text).
#colormap_reverse = 0 ## Whether to invert the color gradient bar (0=normal, 1=invert)
#colormap_low_color = "#006400" ## The color corresponding to the lowest value
#colormap_mid_color = "#FFFF00" ## The color corresponding to the middle value
#colormap_high_color = "#FF0000" ## The color corresponding to the highest value
#background_color = "#B888B8" ## Background color
#upper_outlier_ratio = 0.95 ## Defines the top outlier threshold, values above this scale use the highest color
#lower_outlier_ratio = 0 ## Defines the bottom outlier threshold, below this scale uses the lowest color
#Ymax = ## Manually set the maximum value of the current layer to override the automatic calculation result
#Ymin = ## Manually set the minimum value of the current layer to override the automatic calculation result
#cap_max_value = ## Limit the maximum value
#cap_min_value = ## Limit the minimum minimum limit
```



```

#colormap_nlevels = 8 ## Number of color gradient levels
#track_height = 20 ## The height of the current layer (i.e., the orbital height)
#track_bg_height_ratio = 1 ## Ratio of background height to track_height (0-1)
#log_p = 0 ## Whether to do a 0-log10 conversion of the value (0=no, 1=yes)
#padding_ratio = 0 ## The ratio of vertical spacing of adjacent tracks within the same chromosome
#colormap_legend_sizeratio = ## Gradient bar size scale scaling
#yaxis_tick_show = 0 ## Whether to show Y-axis scale labels (0=hidden, 1=show)
#colormap_legend_show = 1 ## Whether to show color gradient bars (0=hidden, 1=show)
#colormap_legend_shift_x = 0 ## Gradient bar horizontal offset
#colormap_legend_shift_y = 0 ## The vertical offset of the gradient bar
#chr_label_shift_x = 0 ## Lateral offset of chromosomal tags
#chr_label_shift_y = 0 ## Longitudinal offset of chromosomal labels
#chr_label_size_ratio = 1.0 ## Chromosomal label font size ratio (relative to default)
#track_shift_x = 0 ## track layer moves the X value coordinates
#track_shift_y = 0 ## track layer moves the Y value coordinates

##### trackALL. Other uncommon parameters #####
#text-font-size = ## Text font size setting
#track_text_size = 1.0 ## Text font size ratio (relative to default)
#... ### More parameters

##### the parameters of each layer of trackX, inheriting all the parameters of
trackALL #####
#SetParaFor = track2 ## Start processing the layer 2 parameters
#File2 = ## Specify additional input files as data sources
#plot_type = hist ## Drawing type: histogram
#show_columns = File2:5 ## Displays the fifth column of data for File2
#label = "Name" ## The label of the current layer and its styling settings (label_size label_color ....)
#SetParaFor = track3
#plot_type = lines ## Drawing type: lines
#show_columns = File1:5,6 ## Displays the data for columns 5 and 6 of File1

```

7.2 Entering Files

Enter at least one data file. Multiple files can be transferred, and the files can be in compressed **GZ** format, which is compatible with **GZ**

```

File1=path1/in1.file
File2=path2/in2.file.gz
...
FileN=pathx/inX.file

```

The length of the chr is automatically determined based on the information in the first three columns of these files.

7.2.1 Data file (required).

The input format is text format, and the number of columns in each row in the same file must be the same. Make sure that the first three columns are in a fixed format.

In Plot_type file format is as follows:

[ChrName Coordinates 1 Coordinates 2 F lag1Flag2 ...]

If the first line is head, it must start with "#". The software does not require the files to be ordered, but it is recommended to sort the files first (it is recommended that the files be sorted first with sort -k 1,1 -k 2,2n).



4.2.2 Configure color (optional).

The program provides an optional input file, **not required**, that is, a file that allows you to define the configuration color yourself, in a simple format, the color is a hexadecimal HTML color

```
A="#F8F8F3"  
B="#A3FF88"  
C="#FFFFF"  
...  
...
```

Color and value correspondence #####
In this order, it is also emphasized in order: In the absence of custom colors, the colors corresponding to Value are automatically assigned according to the color artboard of 1 [Color Brewer first \(click to see more\)](#), 2 Values and 2 The number of equal colors, 3 the number of Counts of Value, and 4 the maximum and minimum values are automatically assigned according to certain rules. [For more details, click here](#)

chr	Start	End	Flag(Value)
-----	-------	-----	-------------

If the corresponding Flag value only appears (e.g. 1, 2, 1e10...). The program will automatically treat Value as a numerical value (as=numeric), and if other letters appear, it will be treated as a string (as=factor).

For ease of understanding, the default division rules are used

For example, for example

Assuming 9 equal colors, there are 100 Flags, and the statistics frequency of Flags is as follows

01: 10
02: 20
03: 20
04: 20
05: 20
06: 10
80: 4
84: 2
99: 4

So

are all numeric values, which will be regarded as numeric with a maximum of 99 (also passed in by YMax) and a minimum of 01, which can also be passed in by YMin).

At *upper_outlier_ratio = 1*,

01-06 corresponds to color 1 ; 80 and 84 correspond to color 8; And 99 corresponds to color 9

When *upper_outlier_ratio = 0.95*,

84 and 99 have a total of 6 squares more than 5%, so 84 and 99 correspond to the highest color 9, 01-05 corresponds to color 1; 80 corresponds to color 8 ;

are all strings

If a non-numeric word appears in the flag, it is considered a string

If it is a value, it can also be treated as a string by hiding the parameter (**asFlag= factor**).

At *upper_outlier_ratio = 1*,

A total of 9 values are the same, and 9 are divided into colors, so one value corresponds to a color (according to the ascii code), that is, 01 is the color 1, 02 is the color 2... 99 is the color 9

When *upper_outlier_ratio = 0.95*,

The highest 84 and 99 have a total of 6 parties of more than 5%, so 84 and 99 correspond to color 9, and the other 7 values, a total of 8 colors, the color is definitely more than the type of string, that is, according to 7 values 7 equal colors, the latter character corresponds to a color, and finally a total of 8 colors.

For more background color (*background_color*) information, such as (Cancel Leave Only [the Border](#), click here).

7.3 Output Files

Output file	Description
out.svg	Output SVG format diagram
out.png	Output PNG format diagram

See the example diagram given in the application scenario above

8. Examples

There are examples in the above scene diagrams, mine

For specific data formats and configurations, see here:

`./bin/RectChr -InConf in.conf -OutPut out.svg`

Here are 8 application scenario examples, configuration files and input file formats, etc., which only take a few minutes to run.

For details, see the **Basic_Tutorials/example*** and **Scene_Usage/example*** directories in the software

For details, see the data and configuration of example* in the program directory, search for some other people's configurations and schematics on the Internet, click to find the web page, view



General introduction to RectChr

[RectChr of the two populations of the selected signal + selection region](#)

[RectChr is a population genetic polymorphism](#)

[RectChr is selected for several methods](#)

[RectChr of the two populations of the selected signal + selected region horizontally
chr](#)

[RectChr's group sweep + QTLS+IBD map](#)

[RectChr collinearity analysis of two genomes](#)

[RectChr multi-genome \(3 or more\) collinearity analysis](#)

[RectChr multi-sample genotype/gene/haplotype heat map](#)

[RectChr's multi-sample multi-region binmap heat map](#)

[RectChr Dynamic heat maps and dynamic bar charts](#)

[RectChr GWAS Manhattan map with a sense of luxury](#)

More examples can be updated at any time, see the website page, see here:

<https://github.com/hewm2008/RectChr> inside

There are also many articles published in the paper, which can also prove that there are many examples

The screenshot shows a Google Scholar search interface. The search term "rectchr" is typed into the search bar. Below the search bar, there are two main sections: "文章" (Articles) and "找到约 62 条结果 (用时 0.09 秒)" (Found approximately 62 results (in 0.09 seconds)).

9. Advantages

1 Fast and less memory, batch drawing, instant results.

2 You can customize various parameters, such as chr layer, you can define your own color, define the height, and the drawing design is fully open to users, which can be applied in a variety of scenarios

3 Wide range of application scenarios, like CIRCOS, users can draw pictures based on their own data.

4 No installation, easy to use

5 There are at least 54 citations



10. FAQs

10.1 RectChr parameter change condensed

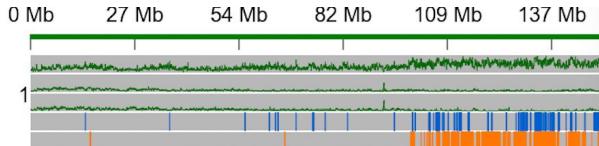
RectChr encountered a lot of needs before 1.39, and has been constantly updating functions and rich parameters, but because it is intermittent, many parameters are not uniformly named, and after 1.39, the parameters are uniformly re-switched, we provide a relationship table of the corresponding parameters of the switch, and in order to facilitate old users to use the previous configuration, we provide ParaOld2New.pl in 1.39. The old configuration can be moved to the new one

```
Perl  ParaOld2New.pl  in_old.conf  out_new.conf
```

10.2 Axis Cancel or Custom Gradient

Cancel the coordinate system, there is a parameter of equal coordinates under global (default 10), and change this one to minus 1 [*axis_tick_num=-1*] or *xaxis_tick_show=0* can cancel the coordinate axis. See RectChr's X axis above for details

10.3 Text Color or Hightline and Other Colors Don't Want to Gradient? How to set it up



Answer: The parameter *colormap_nlevels* in the corresponding level *is* set to 3, and the three-color gradient parameter can be changed to the same color, as follows: the three can be changed to the same color

```
#colormap_nlevels=3
#colormap_low_color = "#006400" ## The color corresponding to the lowest value
#colormap_mid_color = "#FFF000" ## The color corresponding to the middle value
#colormap_high_color = "#FF0000" ## The color corresponding to the highest value
```

10.4 Can I draw a marker on the coordinate axis for line, point, hist, etc.?

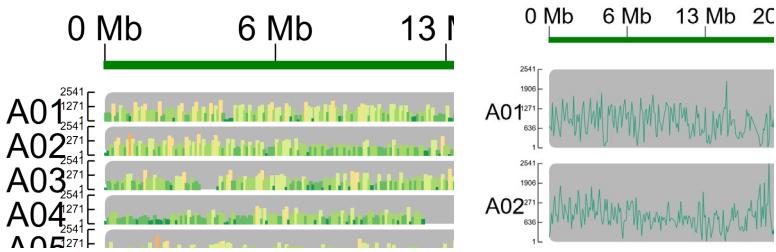
Can you add a value to the left side of the line as shown above?

A: Parameters added after version 1.24

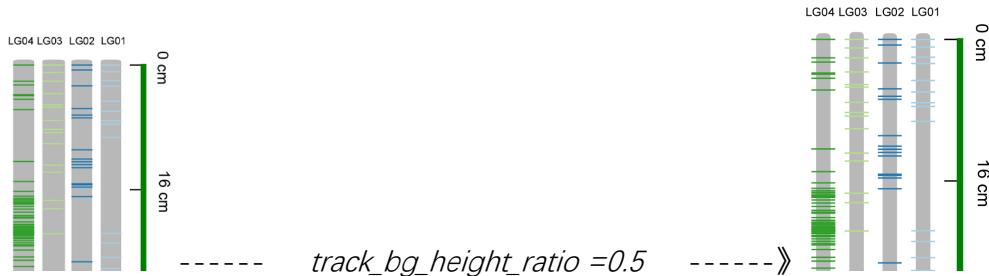
```
yaxis_tick_show=0 ## Displays the start and end values of the Y axis for all layers, the default value of this: 0 is not displayed
```



Put the corresponding layer `yaxis_tick_show=1`, i.e., more `yaxis_tic` properties are shown in the parameter list



10.5 How to Draw a Genetic Map Maker Penetrates the Background.



By default, the width of this background `bg_height` is the same as the `track_height`, as long as it is set to

If you change it to a smaller size, the `bg_height` will shrink to the middle

```
#track_bg_height_ratio = 1 ## Ratio of background height to track_height (0-1)
```

10.6 How to solve the problem of text overlap when drawing text datasets in the same area.

After 1.39, there are new parameters, `track_text_overlap` default is 5, that is, they cannot be stacked together, and only a maximum of 5 texts can be drawn in an area, and if there are many, they will not be drawn. As follows

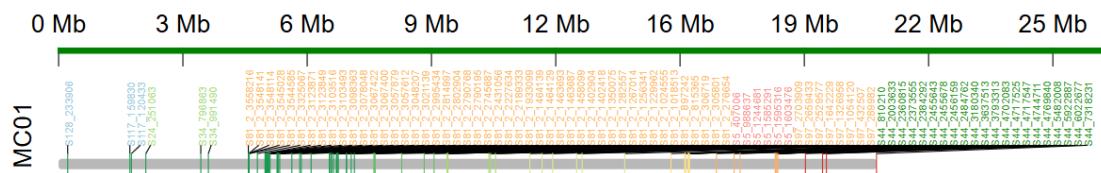


When `track_text_overlap=0` can be stacked, draw all, and the black line will be canceled.



You can also set the track_text_overlap to maximum, which means that all files are listed in an unstacked format

For example, after track_text_overlap=10000



10.7 The length of the chr is wrong, or do you want to draw all the chr?

RectChr records the number and length of chr based on the first three columns. Sometimes I just want to mark a certain area on chr 02, just ch01 has no data, RectChr draws.

For example, File1 has only one line:

```
chr02    5000000 10000000  Flag
```

Then drawing chr01 directly is not drawing, and the length of chr02 will only be drawn to 10M.

There are 2 solutions:

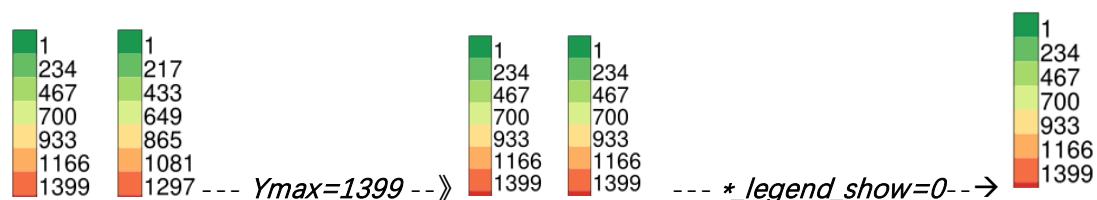
Solution 1: Add [File2 to record the chr length](#), and you don't need to go to File2 for mapping

Scheme 2: Add the length of each chr to File1, and replace Flag with NA (RectChr recognizes NA as unmarked).

10.8 Values for Uniform Legends

For example, the SNP number graph of two samples, because different data are placed in different tracks, the highest and lowest values are different, how to do it, as follows. The usual practice is to unify the highest and lowest levels, and set the same Ymax Ymin on the track corresponding to ALL or

. You can cancel one at the same time (track2 set `colormap_legend_show=0`).



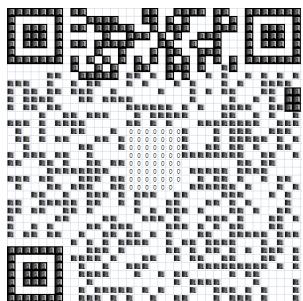
10.9 Contact and Tipping

Casual is fate and blessing, and everything follows the wind

- ✉ hewm2008@gmail.com / hewm2008@qq.com
- join the **QQ Group : 125293663**



WeChat tip QQ to join the group: **125293663 WeChat public account**



群名称:Reseqtools (itools)
群号:125293663

